152241

Delaval, Jan

From: Liu, Samuel
Sent: Monday, May 02, 2005 3:56 PM
To: Delaval, Jan
Subject: 10749387

Hi, Jan,

Please conduct search for the amino acid sequence of SEQ ID NO:1 against commercial **protein** and **interference** databases for application 10749387 east 50 search results, as timely concerned:

Very best,

Samuel Liu
AU 1653, REM 3C84
571-272-0949

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 2, 2005, 15:59:06 ; Search time 74 Seconds
(without alignments)
658.538 Million cell updates/sec

Title: US-10-749-387-1
Perfect score: 695
Sequence: 1 DLECPSGWSSTDRYCYKPFK.....WFKVDCEQQHSFICKFTRPR 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	684	98.4	126	2	AAR71979	Aar71979 Snake ven
2	684	98.4	126	3	AAY85627	Aay85627 Snake ven
3	684	98.4	126	5	AAO20973	Aao20973 126-mer w
4	684	98.4	149	2	AAR71981	Aar71981 Snake ven
5	684	98.4	149	3	AAY85628	Aay85628 Snake ven
6	684	98.4	149	5	AAO20974	Aao20974 149-mer w
7	678	97.6	126	5	AAO20983	Aao20983 M10-G4 K6
8	678	97.6	126	5	AAO20990	Aao20990 M17-G4 R1
9	678	97.6	126	5	AAO20986	Aao20986 M13-G4 R6
10	678	97.6	126	5	AAO20991	Aao20991 M18-G4 R1
11	678	97.6	126	5	AAO20988	Aao20988 M15-G4 R1
12	678	97.6	126	5	AAO20980	Aao20980 M7-G4 K20
13	678	97.6	126	5	AAO20984	Aao20984 M11-G4 E6
14	678	97.6	126	5	AAO20992	Aao20992 M19-G4 E1
15	676	97.3	126	5	AAO20989	Aao20989 M16-G4 D1
16	676	97.3	126	5	AAO20993	Aao20993 M20-G4 F1
17	676	97.3	126	5	AAO20981	Aao20981 M8-G4 D54
18	675	97.1	126	5	AAO20985	Aao20985 M12-G4 Y6
19	675	97.1	126	5	AAO20987	Aao20987 M14-G4 Y6
20	675	97.1	126	5	AAO20982	Aao20982 M9-G4 Y58
21	673	96.8	126	5	AAO20998	Aao20998 M25-G4 D1
22	671	96.5	126	5	AAO20996	Aao20996 M23-G4 D5
23	670	96.4	126	5	AAO20999	Aao20999 M26-G4 D1
24	668	96.1	126	5	AAO20997	Aao20997 M24-G4 D5
25	668	96.1	126	5	AAO20994	Aao20994 M21-G4 D5
26	662	95.3	126	5	AAO20995	Aao20995 M22-G4 D5
27	661	95.1	127	2	AAR24426	Aar24426 Sequence
28	551	79.3	110	5	AAO20975	Aao20975 110-mer c
29	361.5	52.0	158	5	AAE20181	Aae20181 Pigmy rat
30	340.5	49.0	130	2	AAR38228	Aar38228 Sequence
31	322.5	46.4	132	2	AAR38226	Aar38226 Sequence
32	318.5	45.8	131	2	AAR38222	Aar38222 Sequence
33	316.5	45.5	144	5	AAE20180	Aae20180 Pigmy rat
34	314.5	45.3	152	5	AAE20179	Aae20179 Pigmy rat
35	311	44.7	133	2	AAR45156	Aar45156 Botroceti
36	307.5	44.2	134	2	AAR38223	Aar38223 Sequence
37	304.5	43.8	154	5	AAO14520	Aao14520 Korean ad
38	292.5	42.1	152	4	AAM51543	Aam51543 Snake ven
39	274	39.4	132	5	ABB79130	Abb79130 Ahylysant
40	271.5	39.1	129	6	ABU08798	Abu08798 Deinagkis
41	271.5	39.1	129	7	ABU62534	Abu62534 Snake ant
42	262.5	37.8	132	2	AAR72235	Aar72235 Vipera pa
43	256.5	36.9	133	2	AAR38230	Aar38230 Sequence
44	243.5	35.0	123	2	AAR38225	Aar38225 Sequence
45	226.5	32.6	127	2	AAR72236	Aar72236 Vipera pa
46	210.5	30.3	146	4	AAM51544	Aam51544 Snake ven
47	210.5	30.3	146	6	ABU08799	Abu08799 Deinagkis
48	210.5	30.3	146	7	ABU62539	Abu62539 Snake ant
49	209	30.1	116	2	AAR24427	Aar24427 Sequence
50	208	29.9	38	2	AAR71978	Aar71978 Snake ven
51	201.5	29.0	123	5	ABB79131	Abb79131 Ahylysant
52	200	28.8	107	2	AAR38227	Aar38227 Sequence
53	198	28.5	145	5	AAO14521	Aao14521 Korean ad
54	197	28.3	36	2	AAR23885	Aar23885 N-termina
55	191.5	27.6	125	2	AAR45157	Aar45157 Botroceti
56	188.5	27.1	125	2	AAR38224	Aar38224 Sequence
57	184.5	26.5	151	5	AAE20178	Aae20178 Pigmy rat
58	176	25.3	120	5	ABB83143	Abb83143 Ahylysant
59	174	25.0	166	1	AAP81514	Aap81514 Sequence
60	172.5	24.8	34	5	AAO20977	Aao20977 Peptide f
61	172	24.7	44	3	AAY85632	Aay85632 Snake ven
62	172	24.7	165	1	AAP94614	Aap94614 Human reg
63	168	24.2	133	2	AAR66593	Aar66593 Human reg
64	168	24.2	144	2	AAR66592	Aar66592 Human reg
65	168	24.2	146	2	AAR66591	Aar66591 Human reg

ALIGNMENTS

RESULT 1
AAR71979
ID AAR71979 standard; peptide; 126 AA.
XX
AC AAR71979;
XX
DT 25-MAR-2003 (revised)
DT 28-NOV-1995 (first entry)
XX
DE Snake venom derived antithrombotic peptide.
XX
KW Antithrombotic peptide; snake venom; platelet binding inhibition;
KW von Willebrand factors; Crotalus horridus horridus.
XX
OS Crotalus horridus horridus.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 4. .15
FT Disulfide-bond 32. .120
FT Disulfide-bond 95. .112
XX
PN WO9508573-A1.
XX
PD 30-MAR-1995.
XX
PF 21-SEP-1994; 94WO-JP001555.
XX
PR 22-SEP-1993; 93JP-00236975.

XX
PA (AJIN) AJINOMOTO KK.
XX
PI Fukuchi N, Yamamoto H, Nagano M, Kito M, Tanaka A, Ishii K;
PI Kobayashi T, Yoshimoto R;
XX
DR WPI; 1995-139559/18.
XX
PT Single-chain antithrombotic peptide - obtained by cleaving an
PT oligopeptide from snake venom to break inter-chain di:sulphide bonds but
PT preserve intra-chain di:sulphide bonds.
XX
PS Claim 3; Page 44-45; 84pp; Japanese.
XX
CC AAR71978 and AAR71979 are snake venom derived antithrombotic peptides,
CC prepared by cleaving the interpeptide but retaining the intrapeptide
CC disulphide bonds of the original snake venom oligopeptide. These peptides
CC have the advantage of avoiding significant thrombocytopenia when
CC administered at the minimun dose, for in vivo inhibition of platelet von
CC Willebrand factor binding. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 126 AA;

Query Match 98.4%; Score 684; DB 2; Length 126;
Best Local Similarity 98.4%; Pred. No. 1.5e-71;
Matches 124; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
Db 1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy 61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
Db 61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy 121 KFTRPR 126
Db 121 KFTRPR 126

RESULT 2
AAY85627
ID AAY85627 standard; protein; 126 AA.
XX
AC AAY85627;
XX
DT 07-FEB-2001 (first entry)
XX
DE Snake venom derived protein.
XX
KW Subunit peptide production; snake venom; rattlesnake; thrombolytic;
KW von Willebrand's factor; blood platelet-inhibitory activity.
XX
OS Crotalus horridus horridus.
XX
PN WO200059926-A1.
XX
PD 12-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-JP002127.
XX
PR 02-APR-1999; 99JP-00096073.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Fukuchi N, Kageyama S, Kito M, Kayahara T, Yamamoto H;
XX
DR WPI; 2000-664985/64.
XX
PT Producing physiologically-active subunit peptides originating in polymer
PT proteins by denaturation and specific separation, with lower antigenicity
PT but improved solubility and stability, e.g. blood platelet-binding
PT inhibitors.
XX
PS Claim 15; Page 44; 51pp; Japanese.
XX
CC This invention relates to a method for the production of a subunit
CC peptide originating from a polymer protein with disulphide bonds within
CC and between subunits. The method comprises denaturing the protein or its
CC subunit using a protein denaturing agent in a solution, removing the
CC agent in the presence of a polyoxyalkyl polyether which reacts with a
CC thiol group and unwinds the subunit, and separating the polyoxyalkyl
CC polyether-bound subunit peptide. The method can be used for producing
CC physiologically-active subunit peptides for polymer proteins e.g. snake
CC venom-originated dimer peptide with blood platelet-inhibitory activity on
CC von Willebrand's factor. The peptides produced have platelet-binding
CC inhibitory, and thrombolytic activity. The present sequence represents a
CC rattlesnake protein used in an example illustrating the method of the
CC invention
XX
SQ Sequence 126 AA;

Query Match 98.4%; Score 684; DB 3; Length 126;
Best Local Similarity 98.4%; Pred. No. 1.5e-71;
Matches 124; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
Db 1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy 61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
Db 61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy 121 KFTRPR 126
Db 121 KFTRPR 126

RESULT 3
AAO20973
ID AAO20973 standard; protein; 126 AA.
XX
AC AAO20973;
XX
DT 19-JUL-2002 (first entry)
XX
DE 126-mer wild-type rattlesnake protein.
XX
KW Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW drug efficacy.
XX
OS Crotalus horridus horridus.
XX
PN EP1195384-A1.
XX
PD 10-APR-2002.
XX
PF 04-OCT-2001; 2001EP-00123277.
XX
PR 04-OCT-2000; 2000JP-00305279.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
PI Gondoh K, Shimba N, Yamada N;
XX
DR WPI; 2002-364482/40.
XX
PT Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT comprises specific mutations in protein originating from snake venom.
XX
PS Claim 1; Page 25; 49pp; English.
XX
CC The invention relates to a glycoprotein Ib-binding protein, originating

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CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   antithrombotic AS1051 126-mer wild-type rattlesnake protein of the
CC   invention
XX
SQ   Sequence 126 AA;

  Query Match             98.4%;  Score 684;  DB 5;  Length 126;
  Best Local Similarity   98.4%;  Pred. No. 1.5e-71;
  Matches  124;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 4
AAR71981
ID   AAR71981 standard; protein; 149 AA.
XX
AC   AAR71981;
XX
DT   25-MAR-2003  (revised)
DT   28-NOV-1995  (first entry)
XX
DE   Snake venom antithrombotic oligopeptide.
XX
KW   Antithrombotic peptide; snake venom; platelet binding inhibition;
KW   von Willebrand factors; Crotalus horridus horridus.
XX
OS   Crotalus horridus horridus.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  27. .38
FT   Disulfide-bond  55. .143
FT   Disulfide-bond  118. .135
XX
PN   WO9508573-A1.
XX
PD   30-MAR-1995.
XX
PF   21-SEP-1994;   94WO-JP001555.
XX
PR   22-SEP-1993;   93JP-00236975.
XX
PA   (AJIN ) AJINOMOTO KK.
XX
PI   Fukuchi N,  Yamamoto H,  Nagano M,  Kito M,  Tanaka A,  Ishii K;
PI   Kobayashi T,  Yoshimoto R;
XX
DR   WPI; 1995-139559/18.
DR   N-PSDB; AAQ89309.
XX
PT   Single-chain antithrombotic peptide - obtained by cleaving an
PT   oligopeptide from snake venom to break inter-chain di:sulphide bonds but
PT   preserve intra-chain di:sulphide bonds.
XX
PS   Example 2; Page 47-48; 84pp; Japanese.
XX
CC   AAR71978 and AAR71979 are snake venom derived antithrombotic peptides,
CC   specifically from the snake venom oligopeptide AAR71981, encoded by
CC   AAQ89309. These peptides have the advantage of avoiding significant
CC   thrombocytopenia when administered at the minimun dose, for in vivo
CC   inhibition of platelet von Willebrand factor binding. (Updated on 25-MAR-
CC   2003 to correct PN field.)
XX
SQ   Sequence 149 AA;

  Query Match             98.4%;  Score 684;  DB 2;  Length 149;
  Best Local Similarity   98.4%;  Pred. No. 1.8e-71;
  Matches  124;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||
Db         24 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 143

Qy        121 KFTRPR 126
              ||||||
Db        144 KFTRPR 149


RESULT 5
AAY85628
ID   AAY85628 standard; protein; 149 AA.
XX
AC   AAY85628;
XX
DT   07-FEB-2001  (first entry)
XX
DE   Snake venom derived protein.
XX
KW   Subunit peptide production; snake venom; rattlesnake; thrombolytic;
KW   von Willebrand's factor; blood platelet-inhibitory activity.
XX
OS   Crotalus horridus horridus.
XX
PN   WO200059926-A1.
XX
PD   12-OCT-2000.
XX
PF   31-MAR-2000; 2000WO-JP002127.
XX
PR   02-APR-1999;   99JP-00096073.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kageyama S,  Kito M,  Kayahara T,  Yamamoto H;
XX
DR   WPI; 2000-664985/64.
DR   N-PSDB; AAC61144.
XX
PT   Producing physiologically-active subunit peptides originating in polymer
PT   proteins by denaturation and specific separation, with lower antigenicity
PT   but improved solubility and stability, e.g. blood platelet-binding
PT   inhibitors.
XX
PS   Example 2; Page 47; 51pp; Japanese.
XX
CC   This invention relates to a method for the production of a subunit
CC   peptide originating from a polymer protein with disulphide bonds within
CC   and between subunits. The method comprises denaturing the protein or its
CC   subunit using a protein denaturing agent in a solution, removing the
CC   agent in the presence of a polyoxyalkyl polyether which reacts with a
CC   thiol group and unwinds the subunit, and separating the polyoxyalkyl
CC   polyether-bound subunit peptide. The method can be used for producing
CC   physiologically-active subunit peptides for polymer proteins e.g. snake
CC   venom-originated dimer peptide with blood platelet-inhibitory activity on
CC   von Willebrand's factor. The peptides produced have platelet-binding
CC   inhibitory, and thrombolytic activity. The present sequence represents a
CC   rattlesnake protein used in an example illustrating the method of the
CC   invention
```

```
XX
SQ   Sequence 149 AA;

  Query Match             98.4%;  Score 684;  DB 3;  Length 149;
  Best Local Similarity   98.4%;  Pred. No. 1.8e-71;
  Matches  124;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||||| |||||||||||||||||||||||||||||||||
Db         24 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 143

Qy        121 KFTRPR 126
              ||||||
Db        144 KFTRPR 149


RESULT 6
AAO20974
ID   AAO20974 standard; protein; 149 AA.
XX
AC   AAO20974;
XX
DT   19-JUL-2002  (first entry)
XX
DE   149-mer wild-type rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy.
XX
OS   Crotalus horridus horridus.
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
DR   N-PSDB; AAK99834.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 1; Page 26-27; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   antithrombotic 149-mer wild-type rattlesnake protein of the invention
XX
SQ   Sequence 149 AA;

  Query Match             98.4%;  Score 684;  DB 5;  Length 149;
  Best Local Similarity   98.4%;  Pred. No. 1.8e-71;
  Matches  124;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||||| |||||||||||||||||||||||||||||||||

Db         24 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         84 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 143

Qy        121 KFTRPR 126
              ||||||
Db        144 KFTRPR 149


RESULT 7
AAO20983
ID   AAO20983 standard; protein; 126 AA.
XX
AC   AAO20983;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M10-G4 K61A mutant of the antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 61
FT                   /note= "Wild-type Lys substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 4; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   K61A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC   protein of the invention. NOTE: This mutant protein sequence is not shown
CC   in the specification. It has been created from information provided in
CC   Example 4
XX
SQ   Sequence 126 AA;

  Query Match             97.6%;  Score 678;  DB 5;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 7.4e-71;
  Matches  123;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
```

```
Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126
```

RESULT 8
AAO20990
ID AAO20990 standard; protein; 126 AA.
XX
AC AAO20990;
XX
DT 19-JUL-2002 (first entry)
XX
DE M17-G4 R103A mutant of the antithrombotic rattlesnake protein.
XX
KW Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW drug efficacy; mutant; mutein.
XX
OS Crotalus horridus horridus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 103
FT /note= "Wild-type Arg substituted by Ala"
XX
PN EP1195384-A1.
XX
PD 10-APR-2002.
XX
PF 04-OCT-2001; 2001EP-00123277.
XX
PR 04-OCT-2000; 2000JP-00305279.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
PI Gondoh K, Shimba N, Yamada N;
XX
DR WPI; 2002-364482/40.
XX
PT Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT comprises specific mutations in protein originating from snake venom.
XX
PS Example 4; Page; 49pp; English.
XX
CC The invention relates to a glycoprotein Ib-binding protein, originating
CC from snake venom, comprising specific mutations and antithrombotic
CC activity. Glycoprotein Ib-binding protein is used in a drug having
CC antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC binding activity to glycoprotein Ib, a long half life/drug efficacy
CC retention in blood, and low antigenicity. This sequence represents the
CC R103A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC protein of the invention. NOTE: This mutant protein sequence is not shown
CC in the specification. It has been created from information provided in
CC Example 4
XX
SQ Sequence 126 AA;

```
  Query Match             97.6%;  Score 678;  DB 5;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 7.4e-71;
  Matches  123;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTALREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126
```

RESULT 9
AAO20986
ID AAO20986 standard; protein; 126 AA.
XX
AC AAO20986;
XX
DT 19-JUL-2002 (first entry)
XX
DE M13-G4 R66A mutant of the antithrombotic rattlesnake protein.
XX
KW Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW drug efficacy; mutant; mutein.
XX
OS Crotalus horridus horridus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 66
FT /note= "Wild-type Arg substituted by Ala"
XX
PN EP1195384-A1.
XX
PD 10-APR-2002.
XX
PF 04-OCT-2001; 2001EP-00123277.
XX
PR 04-OCT-2000; 2000JP-00305279.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
PI Gondoh K, Shimba N, Yamada N;
XX
DR WPI; 2002-364482/40.
XX
PT Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT comprises specific mutations in protein originating from snake venom.
XX
PS Example 4; Page; 49pp; English.
XX
CC The invention relates to a glycoprotein Ib-binding protein, originating
CC from snake venom, comprising specific mutations and antithrombotic
CC activity. Glycoprotein Ib-binding protein is used in a drug having
CC antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC binding activity to glycoprotein Ib, a long half life/drug efficacy
CC retention in blood, and low antigenicity. This sequence represents the
CC R66A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC protein of the invention. NOTE: This mutant protein sequence is not shown
CC in the specification. It has been created from information provided in
CC Example 4
XX
SQ Sequence 126 AA;

```
  Query Match             97.6%;  Score 678;  DB 5;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 7.4e-71;
  Matches  123;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEYLTAYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
```

```
Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 10
AAO20991
ID   AAO20991 standard; protein; 126 AA.
XX
AC   AAO20991;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M18-G4 R105A mutant of the antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 105
FT                   /note= "Wild-type Arg substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 4; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   R105A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC   protein of the invention. NOTE: This mutant protein sequence is not shown
CC   in the specification. It has been created from information provided in
CC   Example 4
XX
SQ   Sequence 126 AA;

  Query Match             97.6%;  Score 678;  DB 5;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 7.4e-71;
  Matches  123;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLAEWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 11
AAO20988
ID   AAO20988 standard; protein; 126 AA.
XX
AC   AAO20988;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M15-G4 R100A mutant of the antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 100
FT                   /note= "Wild-type Arg substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 4; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   R100A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC   protein of the invention. NOTE: This mutant protein sequence is not shown
CC   in the specification. It has been created from information provided in
CC   Example 4
XX
SQ   Sequence 126 AA;

  Query Match             97.6%;  Score 678;  DB 5;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 7.4e-71;
  Matches  123;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSADTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126
```

```
RESULT 12
AAO20980
ID   AAO20980 standard; protein; 126 AA.
XX
AC   AAO20980;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M7-G4 K20A mutant of the antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 20
FT                   /note= "Wild-type Lys substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 4; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   K20A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC   protein of the invention. NOTE: This mutant protein sequence is not shown
CC   in the specification. It has been created from information provided in
CC   Example 4
XX
SQ   Sequence 126 AA;

  Query Match             97.6%;  Score 678;  DB 5;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 7.4e-71;
  Matches  123;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| |||||||| |||||| ||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFAQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 13
AAO20984
ID   AAO20984 standard; protein; 126 AA.
XX
AC   AAO20984;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M11-G4 E62A mutant of the antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 62
FT                   /note= "Wild-type Glu substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 4; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   E62A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC   protein of the invention. NOTE: This mutant protein sequence is not shown
CC   in the specification. It has been created from information provided in
CC   Example 4
XX
SQ   Sequence 126 AA;

  Query Match             97.6%;  Score 678;  DB 5;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 7.4e-71;
  Matches  123;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| |||||||| |||||| ||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KAYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 14
AAO20992
ID   AAO20992 standard; protein; 126 AA.
```

XX
AC AAO20992;
XX
DT 19-JUL-2002 (first entry)
XX
DE M19-G4 E106A mutant of the antithrombotic rattlesnake protein.
XX
KW Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW drug efficacy; mutant; mutein.
XX
OS Crotalus horridus horridus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 106
FT /note= "Wild-type Glu substituted by Ala"
XX
PN EP1195384-A1.
XX
PD 10-APR-2002.
XX
PF 04-OCT-2001; 2001EP-00123277.
XX
PR 04-OCT-2000; 2000JP-00305279.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
PI Gondoh K, Shimba N, Yamada N;
XX
DR WPI; 2002-364482/40.
XX
PT Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT comprises specific mutations in protein originating from snake venom.
XX
PS Example 4; Page; 49pp; English.
XX
CC The invention relates to a glycoprotein Ib-binding protein, originating
CC from snake venom, comprising specific mutations and antithrombotic
CC activity. Glycoprotein Ib-binding protein is used in a drug having
CC antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC binding activity to glycoprotein Ib, a long half life/drug efficacy
CC retention in blood, and low antigenicity. This sequence represents the
CC E106A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC protein of the invention. NOTE: This mutant protein sequence is not shown
CC in the specification. It has been created from information provided in
CC Example 4
XX
SQ Sequence 126 AA;

Query Match 97.6%; Score 678; DB 5; Length 126;
Best Local Similarity 97.6%; Pred. No. 7.4e-71;
Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              ||||||||||  ||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLRAWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126
```

RESULT 15
AAO20989
ID AAO20989 standard; protein; 126 AA.
XX
AC AAO20989;
XX
DT 19-JUL-2002 (first entry)
XX
DE M16-G4 D101A mutant of the antithrombotic rattlesnake protein.
XX
KW Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW drug efficacy; mutant; mutein.
XX
OS Crotalus horridus horridus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 101
FT /note= "Wild-type Asp substituted by Ala"
XX
PN EP1195384-A1.
XX
PD 10-APR-2002.
XX
PF 04-OCT-2001; 2001EP-00123277.
XX
PR 04-OCT-2000; 2000JP-00305279.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
PI Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
PI Gondoh K, Shimba N, Yamada N;
XX
DR WPI; 2002-364482/40.
XX
PT Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT comprises specific mutations in protein originating from snake venom.
XX
PS Example 4; Page; 49pp; English.
XX
CC The invention relates to a glycoprotein Ib-binding protein, originating
CC from snake venom, comprising specific mutations and antithrombotic
CC activity. Glycoprotein Ib-binding protein is used in a drug having
CC antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC binding activity to glycoprotein Ib, a long half life/drug efficacy
CC retention in blood, and low antigenicity. This sequence represents the
CC D101A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC protein of the invention. NOTE: This mutant protein sequence is not shown
CC in the specification. It has been created from information provided in
CC Example 4
XX
SQ Sequence 126 AA;

Query Match 97.3%; Score 676; DB 5; Length 126;
Best Local Similarity 97.6%; Pred. No. 1.3e-70;
Matches 123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              ||||||||||  ||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRATRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126
```

RESULT 16
AAO20993
ID AAO20993 standard; protein; 126 AA.
XX
AC AAO20993;
XX
DT 19-JUL-2002 (first entry)

```
XX
DE   M20-G4 F108A mutant of the antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 108
FT                   /note= "Wild-type Phe substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 4; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   F108A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC   protein of the invention. NOTE: This mutant protein sequence is not shown
CC   in the specification. It has been created from information provided in
CC   Example 4
XX
SQ   Sequence 126 AA;

  Query Match             97.3%;  Score 676;  DB 5;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 1.3e-70;
  Matches  123;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              ||||||||||  |||||||||||||||  |||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWAKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 17
AAO20981
ID   AAO20981 standard; protein; 126 AA.
XX
AC   AAO20981;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M8-G4 D54A mutant of the antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 54
FT                   /note= "Wild-type Asp substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 4; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   D54A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC   protein of the invention. NOTE: This mutant protein sequence is not shown
CC   in the specification. It has been created from information provided in
CC   Example 4
XX
SQ   Sequence 126 AA;

  Query Match             97.3%;  Score 676;  DB 5;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 1.3e-70;
  Matches  123;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              ||||||||||  |||||||||||||||  |||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVANVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 18
AAO20985
ID   AAO20985 standard; protein; 126 AA.
XX
AC   AAO20985;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M12-G4 Y63A mutant of the antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
```

```
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 63
FT                   /note= "Wild-type Tyr substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 4; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   Y63A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC   protein of the invention. NOTE: This mutant protein sequence is not shown
CC   in the specification. It has been created from information provided in
CC   Example 4
XX
SQ   Sequence 126 AA;

  Query Match             97.1%;  Score 675;  DB 5;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 1.6e-70;
  Matches  123;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEALTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 19
AAO20987
ID   AAO20987 standard; protein; 126 AA.
XX
AC   AAO20987;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M14-G4 Y67A mutant of the antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 67
FT                   /note= "Wild-type Tyr substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 4; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   Y67A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC   protein of the invention. NOTE: This mutant protein sequence is not shown
CC   in the specification. It has been created from information provided in
CC   Example 4
XX
SQ   Sequence 126 AA;

  Query Match             97.1%;  Score 675;  DB 5;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 1.6e-70;
  Matches  123;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEYLTRAIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 20
AAO20982
ID   AAO20982 standard; protein; 126 AA.
XX
AC   AAO20982;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M9-G4 Y58A mutant of the antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 58
FT                   /note= "Wild-type Tyr substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 4; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   Y58A mutant of the antithrombotic AS1051 126-mer wild-type rattlesnake
CC   protein of the invention. NOTE: This mutant protein sequence is not shown
CC   in the specification. It has been created from information provided in
CC   Example 4
XX
SQ   Sequence 126 AA;

  Query Match             97.1%;  Score 675;  DB 5;  Length 126;
  Best Local Similarity   97.6%;  Pred. No. 1.6e-70;
  Matches  123;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||||| |||||||||||||||||||||||||||| ||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLAAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 21
AAO20998
ID   AAO20998 standard; protein; 126 AA.
XX
AC   AAO20998;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M25-G4 D101A, E106Q mutant of antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
```

```
FH   Key             Location/Qualifiers
FT   Misc-difference 101
FT                   /note= "Wild-type Asp substituted by Ala"
FT   Misc-difference 106
FT                   /note= "Wild-type Glu substituted by Gln"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 6; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   D101A, E106Q mutant of the antithrombotic AS1051 126-mer wild-type
CC   rattlesnake protein of the invention. NOTE: This mutant protein sequence
CC   is not shown in the specification. It has been created from information
CC   provided in Example 6
XX
SQ   Sequence 126 AA;

  Query Match             96.8%;  Score 673;  DB 5;  Length 126;
  Best Local Similarity   96.8%;  Pred. No. 2.8e-70;
  Matches  122;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||||||||||||||| |||||:|||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRATRLRQWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 22
AAO20996
ID   AAO20996 standard; protein; 126 AA.
XX
AC   AAO20996;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M23-G4 D54N, D101A mutant of antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
```

```
FH   Key             Location/Qualifiers
FT   Misc-difference 54
FT                   /note= "Wild-type Asp substituted by Asn"
FT   Misc-difference 101
FT                   /note= "Wild-type Asp substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 6; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   D54N, D101A mutant of the antithrombotic AS1051 126-mer wild-type
CC   rattlesnake protein of the invention. NOTE: This mutant protein sequence
CC   is not shown in the specification. It has been created from information
CC   provided in Example 6
XX
SQ   Sequence 126 AA;

  Query Match             96.5%;  Score 671;  DB 5;  Length 126;
  Best Local Similarity   96.8%;  Pred. No. 4.8e-70;
  Matches  122;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| |||||||||||||| |||||||||||||||||||:||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVNNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRATRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 23
AAO20999
ID   AAO20999 standard; protein; 126 AA.
XX
AC   AAO20999;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M26-G4 D101A, E106A mutant of antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
```

```
FH   Key             Location/Qualifiers
FT   Misc-difference 101
FT                   /note= "Wild-type Asp substituted by Ala"
FT   Misc-difference 106
FT                   /note= "Wild-type Glu substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 6; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   D101A, E106A mutant of the antithrombotic AS1051 126-mer wild-type
CC   rattlesnake protein of the invention. NOTE: This mutant protein sequence
CC   is not shown in the specification. It has been created from information
CC   provided in Example 6
XX
SQ   Sequence 126 AA;

  Query Match             96.4%;  Score 670;  DB 5;  Length 126;
  Best Local Similarity   96.8%;  Pred. No. 6.3e-70;
  Matches  122;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||||||||||||||| |||| ||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRATRLRAWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 24
AAO20997
ID   AAO20997 standard; protein; 126 AA.
XX
AC   AAO20997;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M24-G4 D54A, D101A mutant of antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
```

```
FH   Key             Location/Qualifiers
FT   Misc-difference 54
FT                   /note= "Wild-type Asp substituted by Ala"
FT   Misc-difference 101
FT                   /note= "Wild-type Asp substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 6; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   D54A, D101A mutant of the antithrombotic AS1051 126-mer wild-type
CC   rattlesnake protein of the invention. NOTE: This mutant protein sequence
CC   is not shown in the specification. It has been created from information
CC   provided in Example 6
XX
SQ   Sequence 126 AA;

  Query Match             96.1%;  Score 668;  DB 5;  Length 126;
  Best Local Similarity   96.8%;  Pred. No. 1.1e-69;
  Matches  122;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||||| |||||||||||||||||||||||||| ||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVANVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRATRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 25
AAO20994
ID   AAO20994 standard; protein; 126 AA.
XX
AC   AAO20994;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M21-G4 D54A, D101N, E106Q mutant of antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
```

```
FH   Key             Location/Qualifiers
FT   Misc-difference 54
FT                   /note= "Wild-type Asp substituted by Ala"
FT   Misc-difference 101
FT                   /note= "Wild-type Asp substituted by Asn"
FT   Misc-difference 106
FT                   /note= "Wild-type Glu substituted by Gln"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 6; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   D54A, D101N, E106Q mutant of the antithrombotic AS1051 126-mer wild-type
CC   rattlesnake protein of the invention. NOTE: This mutant protein sequence
CC   is not shown in the specification. It has been created from information
CC   provided in Example 6
XX
SQ   Sequence 126 AA;

  Query Match             96.1%;  Score 668;  DB 5;  Length 126;
  Best Local Similarity   96.0%;  Pred. No. 1.1e-69;
  Matches  121;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||||| |||||||||||||||||||||||||| ||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVANVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||||||||||||||||||:||||:|||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRNTRLRQWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 26
AAO20995
ID   AAO20995 standard; protein; 126 AA.
XX
AC   AAO20995;
XX
DT   19-JUL-2002  (first entry)
XX
DE   M22-G4 D54A, D101A, E106A mutant of antithrombotic rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; mutant; mutein.
XX
OS   Crotalus horridus horridus.
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 54
FT                   /note= "Wild-type Asp substituted by Ala"
FT   Misc-difference 101
FT                   /note= "Wild-type Asp substituted by Ala"
FT   Misc-difference 106
FT                   /note= "Wild-type Glu substituted by Ala"
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 6; Page; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   D54A, D101A, E106A mutant of the antithrombotic AS1051 126-mer wild-type
CC   rattlesnake protein of the invention. NOTE: This mutant protein sequence
CC   is not shown in the specification. It has been created from information
CC   provided in Example 6
XX
SQ   Sequence 126 AA;

  Query Match             95.3%;  Score 662;  DB 5;  Length 126;
  Best Local Similarity   96.0%;  Pred. No. 5.5e-69;
  Matches  121;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              ||||||||| ||||||||||||| |||||||||||||||||||||| ||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVANVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||||||||||||||| |||| |||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRATRLRAWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 27
AAR24426
ID   AAR24426 standard; protein; 127 AA.
XX
AC   AAR24426;
XX
DT   25-MAR-2003  (revised)
DT   21-NOV-1992  (first entry)
XX
DE   Sequence of the platelet glycoprotein GPIb inhibitor alpha chain (CHH-B-
DE   alpha).
XX
KW   Platelet adherence inhibitor; platelet anti-adhesive;
KW   antithrombotic agent; von Willebrand Factor;
KW   platelet glycoprotein GPIb-IX complex.
XX
OS   Crotalus horridus horridus.
XX
PN   WO9208472-A1.
XX
PD   29-MAY-1992.
XX
PF   14-NOV-1991;   91WO-US008516.
XX
PR   16-NOV-1990;   90US-00614443.
XX
PA   (CORT-) COR THERAPEUTICS INC.
XX
PI   Scarborough RM;
XX
DR   WPI; 1992-199936/24.
XX
PT   Platelet antiadhesive peptide(s) obtd. from snake venom - also inhibit
PT   thrombus formation; for treatment of arteriosclerosis, atherosclerosis,
PT   acute myocardial infarction, chronic unstable angina, etc.
XX
PS   Example; Fig 6; 5pp; English.
XX
CC   The PAA was purified from a solution of snake venom. Analysis of the peak
CC   inhibitory fractions by SDS-PAGE revealed 2 major proteins migrating with
CC   a mol. wt. 23-28 kD. Both were able to inhibit botrocetin and ristocetin
CC   induced platelet agglutination. They were called CHH-A and CHH-B. The
CC   earlier eluting subunit (CHH-B-beta) and later eluting subunit (CHH-B-
CC   alpha) were individually submitted to N-terminal sequence analysis. The
CC   complete amino acid sequence for the alpha and beta chains are given in
CC   AAR24426 and AAR24427. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 127 AA;

  Query Match             95.1%;  Score 661;  DB 2;  Length 127;
  Best Local Similarity   96.0%;  Pred. No. 7.2e-69;
  Matches  121;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              ||||||||| ||||||||||||| |||||||||||||||||||||| ||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGRHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSIYSENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 28
AAO20975
ID   AAO20975 standard; protein; 110 AA.
XX
AC   AAO20975;
XX
DT   19-JUL-2002  (first entry)
XX
DE   110-mer central loop-deficient rattlesnake protein.
XX
KW   Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
KW   antithrombotic; glycoprotein Ib; long half life; low antigenicity;
KW   drug efficacy; loop-deficient.
XX
OS   Crotalus horridus horridus.
OS   Synthetic.
XX
PN   EP1195384-A1.
XX
PD   10-APR-2002.
```

```
XX
PF   04-OCT-2001; 2001EP-00123277.
XX
PR   04-OCT-2000; 2000JP-00305279.
XX
PA   (AJIN ) AJINOMOTO CO INC.
XX
PI   Fukuchi N,  Kito M,  Kayahara T,  Futaki F,  Ishikawa K,  Suzuki E;
PI   Gondoh K,  Shimba N,  Yamada N;
XX
DR   WPI; 2002-364482/40.
XX
PT   Glycoprotein Ib-binding protein, useful for treating thrombosis,
PT   comprises specific mutations in protein originating from snake venom.
XX
PS   Example 2; Page 28; 49pp; English.
XX
CC   The invention relates to a glycoprotein Ib-binding protein, originating
CC   from snake venom, comprising specific mutations and antithrombotic
CC   activity. Glycoprotein Ib-binding protein is used in a drug having
CC   antithrombotic activity. Glycoprotein Ib-binding protein has a high
CC   binding activity to glycoprotein Ib, a long half life/drug efficacy
CC   retention in blood, and low antigenicity. This sequence represents the
CC   110-mer central loop-deficient rattlesnake protein relating to the
CC   invention
XX
SQ   Sequence 110 AA;

  Query Match             79.3%;  Score 551;  DB 5;  Length 110;
  Best Local Similarity   82.5%;  Pred. No. 4.3e-56;
  Matches  104;  Conservative    0;  Mismatches    6;  Indels   16;  Gaps    1;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||                  ||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRGGGG---------------ECFMVSRDTRLREWFKVDCEQQHSFIC 104

Qy        121 KFTRPR 126
              ||||||
Db        105 KFTRPR 110


RESULT 29
AAE20181
ID   AAE20181 standard; protein; 158 AA.
XX
AC   AAE20181;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Pigmy rattlesnake venom gland protein, Zsnk5.
XX
KW   Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
KW   platelet aggregation; Zsnk5.
XX
OS   Sistrurus miliarius.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT   Protein         24. .158
FT                   /label= Mature_Zsnk5_protein
FT   Disulfide-bond  27. .38
FT   Disulfide-bond  55. .152
FT   Disulfide-bond  127. .144
XX
PN   WO200214364-A2.
XX
PD   21-FEB-2002.
XX
PF   13-AUG-2001; 2001WO-US025310.
XX
PR   14-AUG-2000; 2000US-0225072P.
PR   14-AUG-2000; 2000US-0225087P.
PR   15-AUG-2000; 2000US-0225489P.
PR   15-AUG-2000; 2000US-0225490P.
PR   20-DEC-2000; 2000US-0256997P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sheppard PO,  Bishop PD;
XX
DR   WPI; 2002-269180/31.
DR   N-PSDB; AAD32059.
XX
PT   New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which
PT   affect blood coagulation and platelet aggregation system, useful in
PT   therapy and diagnostics, or as tools in the study of genetics or
PT   molecular biology.
XX
PS   Claim 3; Page 3; 79pp; English.
XX
CC   The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
CC   venom gland proteins, which affect blood coagulation and platelet
CC   aggregation system. The polypeptides, which affect blood coagulation and
CC   platelet aggregation system, are useful in therapy and diagnostics. The
CC   polypeptides are also useful as an educational tool in laboratory
CC   practical kits for courses related to genetics and molecular biology,
CC   protein chemistry and antibody production and analysis. The
CC   polynucleotide or polypeptide can be used as standards or as unknowns for
CC   testing purposes. The polypeptides are also useful in identifying
CC   proteins by western blotting, protein purification, determining the
CC   weight of expressed polypeptides as a ratio to total protein expressed,
CC   identifying peptide cleavage sites, coupling amino and carboxyl terminal
CC   tags, mass spectrometry, circular dichroism to determine conformation or
CC   affinity chromatography columns to purify the protein, cloning or
CC   sequencing. The present sequence is Sistrurus miliarius venom gland
CC   protein, Zsnk5
XX
SQ   Sequence 158 AA;

  Query Match             52.0%;  Score 361.5;  DB 5;  Length 158;
  Best Local Similarity   50.4%;  Pred. No. 9.6e-34;
  Matches   66;  Conservative   21;  Mismatches   35;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  ||||| : |:|||:  |:  ||  |||||||||||||| |||   || |:  :: ||
Db         24 DFNCPSGWFAYDQYCYRVIKRLKTWDDAERFCSEQAKGGHLASVENDEEAVFLAQLVAAN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
                :    |:|||||:|||| |       ||:||||||     :|| : ::|   :|:  |
Db         84 IKQNQYYVWIGLRIQNKGQQCSTKWSDGSSVSYENLVKSHSKKCFGLKKETEFLQWYNTD 143

Qy        112 CEQQHSFICKF 122
              ||::: |:|||
Db        144 CEEKNLFVCKF 154


RESULT 30
AAR38228
ID   AAR38228 standard; protein; 130 AA.
XX
AC   AAR38228;
XX
DT   25-MAR-2003  (revised)
DT   01-OCT-1993  (first entry)
XX
DE   Sequence of polypeptide chain of alboaggregin B1 (AL-B2).
XX
KW   Venom; snake; platelet-binding protein.
XX
OS   Trimeresurus albolabris.
XX
```

PN WO9311151-A1.
XX
PD 10-JUN-1993.
XX
PF 01-DEC-1992; 92WO-US010344.
XX
PR 03-DEC-1991; 91US-00803630.
PR 05-JUN-1992; 92US-00893929.
XX
PA (UTEM) UNIV TEMPLE.
XX
PI Kirby EP, Peng M;
XX
DR WPI; 1993-196991/24.
XX
PT New platelet-binding proteins obtained from snake venom - inhibit binding
PT of von Willebrand factor to platelet membrane glycoprotein IB, useful in
PT therapy, diagnosis and surgery.
XX
PS Claim 8; Page 48; 74pp; English.
XX
CC Alboaggregin B1 and B2 (collectively "AL-B"), may be obtained in
CC substantially pure chemical form from venom. Each of AL-B11 and -B2
CC comprise an about 23 kDa protein formed by an about 17 kDa polypeptide
CC chain crosslinked to an about 14 kDa polypeptide chain by one or more
CC interchain disulfide bonds. Each of the two polypeptide chains of AL-B1
CC and -B2 show strong homology to two of the chains of AL-A. AL-B1 and -B2
CC each comprise two non-identical polypeptide chains. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 130 AA;

Query Match 49.0%; Score 340.5; DB 2; Length 130;
Best Local Similarity 50.8%; Pred. No. 2.1e-31;
Matches 66; Conservative 22; Mismatches 29; Indels 13; Gaps 4;

```
Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN-K 61
              :||| |||  :|||:  |:  ||  |||||||||  |||:|:|:  || ||  :|  | |
Db          1 DCPSDWSSFKQYCYQIVKELKTWEDAERFCSEQANDGHLVSIESYREAVFVAELLSENVK 60

Qy         62 EYLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDC 112
              :|   ::|||| |||||| |       ||:||||||  :| :||:: :::  : |  | |
Db         61 KY---HVWIGLSVQNKGQQCSSEWSDGSSVSYENLVKPNPKKCFVLKKESEFKTWSNVYC 117

Qy        113 EQQHSFICKF 122
              ||:| |:|||
Db        118 EQKHIFMCKF 127
```

RESULT 31
AAR38226
ID AAR38226 standard; protein; 132 AA.
XX
AC AAR38226;
XX
DT 25-MAR-2003 (revised)
DT 01-OCT-1993 (first entry)
XX
DE Sequence of polypeptide chain of alboaggregin B1 (AL-B1).
XX
KW Venom; snake; platelet-binding protein.
XX
OS Trimeresurus albolabris.
XX
PN WO9311151-A1.
XX
PD 10-JUN-1993.
XX
PF 01-DEC-1992; 92WO-US010344.
XX
PR 03-DEC-1991; 91US-00803630.
PR 05-JUN-1992; 92US-00893929.
XX
PA (UTEM) UNIV TEMPLE.
XX
PI Kirby EP, Peng M;
XX
DR WPI; 1993-196991/24.
XX
PT New platelet-binding proteins obtained from snake venom - inhibit binding
PT of von Willebrand factor to platelet membrane glycoprotein IB, useful in
PT therapy, diagnosis and surgery.
XX
PS Claim 6; Page 47; 74pp; English.
XX
CC Alboaggregin B1 and B2 (collectively "AL-B"), may be obtained in
CC substantially pure chemical form from venom. Each of AL-B11 and -B2
CC comprise an about 23 kDa protein formed by an about 17 kDa polypeptide
CC chain crosslinked to an about 14 kDa polypeptide chain by one or more
CC interchain disulfide bonds. Each of the two polypeptide chains of AL-B1
CC and -B2 show strong homology to two of the chains of AL-A. AL-B1 and -B2
CC each comprise two non-identical polypeptide chains. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 132 AA;

Query Match 46.4%; Score 322.5; DB 2; Length 132;
Best Local Similarity 47.3%; Pred. No. 2.7e-29;
Matches 61; Conservative 21; Mismatches 38; Indels 9; Gaps 2;

```
Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| |||  :|||:  |:  ||  || ||||||  |||:|:|:  || ||  :|  | :
Db          1 DCPSDWSSFKQYCYQIVKELKTWEDAEXFCSEQANDGHLVSIESYREAVFVAELLSENVK 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                 :|||| |||| | |       ||: ||||:  :| :||:: :::  | |  | ||
Db         61 TTKYNVWIGLSVQNKEQQCSSEWSDGSSVXYENLIKPNPKKCFVLKKESEFRTWSNVYCE 120

Qy        114 QQHSFICKF 122
              |:| |:|||
Db        121 QKHIFMCKF 129
```

RESULT 32
AAR38222
ID AAR38222 standard; protein; 131 AA.
XX
AC AAR38222;
XX
DT 25-MAR-2003 (revised)
DT 01-OCT-1993 (first entry)
XX
DE Sequence of polypeptide chain of alboaggregin A (AL-A).
XX
KW Venom; snake; platelet-binding protein.
XX
OS Trimeresurus albolabris.
XX
PN WO9311151-A1.
XX
PD 10-JUN-1993.
XX
PF 01-DEC-1992; 92WO-US010344.
XX
PR 03-DEC-1991; 91US-00803630.
PR 05-JUN-1992; 92US-00893929.
XX
PA (UTEM) UNIV TEMPLE.
XX
PI Kirby EP, Peng M;
XX
DR WPI; 1993-196991/24.
XX
PT New platelet-binding proteins obtained from snake venom - inhibit binding
PT of von Willebrand factor to platelet membrane glycoprotein IB, useful in
PT therapy, diagnosis and surgery.

```
XX
PS   Claim 4; Page 45; 74pp; English.
XX
CC   AL-A may be obtd. from snake venom. It has a mol. wt. of about 45 kDa. AL
CC   -A contains two types of polypeptide chains, with mol. wt. of about 18
CC   kDa and about 15 kDa, respectively. Each of these two types of chains is
CC   actually composed of two subtypes. Thus, AL-A comprises four non-
CC   identical polypeptide chains. A possible variation of AAR38224 has been
CC   found, characterised by Asp at posn. three in lieu of Cys. (Updated on 25
CC   -MAR-2003 to correct PN field.)
XX
SQ   Sequence 131 AA;

  Query Match             45.8%;  Score 318.5;  DB 2;  Length 131;
  Best Local Similarity   45.0%;  Pred. No. 8e-29;
  Matches   59;  Conservative   22;  Mismatches   41;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| |:|||: ||:  ||  ||||||:||  |||:|:|:| || ||  ::  |
Db          1 DCPSDWSSYDQYCYRVFKRLQTWEDAERFCSQQANDGHLVSIESAGEADFVTQLVSENIR 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVD--PFECFMVSRDTRLREWFKVDCE 113
                 |:||||||| ||| |       ||: ::|| :    :|: : :    | |  | |
Db         61 SEKHYVWIGLRVQGKGQQCSSEWSDGSSVHWDNLQEKNTRKCYGLEKRAEFRTWSNVYCG 120

Qy        114 QQHSFICKFTR 124
               :: |:||| |
Db        121 HEYPFVCKFXR 131


RESULT 33
AAE20180
ID   AAE20180 standard; protein; 144 AA.
XX
AC   AAE20180;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Pigmy rattlesnake venom gland protein, Zsnk4.
XX
KW   Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
KW   platelet aggregation; Zsnk4.
XX
OS   Sistrurus miliarius.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .9
FT                   /label= Signal_peptide
FT   Protein         10. .144
FT                   /label= Mature_Zsnk4_protein
FT   Disulfide-bond  13. .24
FT   Disulfide-bond  41. .138
FT   Disulfide-bond  113. .130
XX
PN   WO200214364-A2.
XX
PD   21-FEB-2002.
XX
PF   13-AUG-2001; 2001WO-US025310.
XX
PR   14-AUG-2000; 2000US-0225072P.
PR   14-AUG-2000; 2000US-0225087P.
PR   15-AUG-2000; 2000US-0225489P.
PR   15-AUG-2000; 2000US-0225490P.
PR   20-DEC-2000; 2000US-0256997P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sheppard PO,  Bishop PD;
XX
DR   WPI; 2002-269180/31.
DR   N-PSDB; AAD32057.
XX
PT   New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which
PT   affect blood coagulation and platelet aggregation system, useful in
PT   therapy and diagnostics, or as tools in the study of genetics or
PT   molecular biology.
XX
PS   Claim 3; Page 3; 79pp; English.
XX
CC   The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
CC   venom gland proteins, which affect blood coagulation and platelet
CC   aggregation system. The polypeptides, which affect blood coagulation and
CC   platelet aggregation system, are useful in therapy and diagnostics. The
CC   polypeptides are also useful as an educational tool in laboratory
CC   practical kits for courses related to genetics and molecular biology,
CC   protein chemistry and antibody production and analysis. The
CC   polynucleotide or polypeptide can be used as standards or as unknowns for
CC   testing purposes. The polypeptides are also useful in identifying
CC   proteins by western blotting, protein purification, determining the
CC   weight of expressed polypeptides as a ratio to total protein expressed,
CC   identifying peptide cleavage sites, coupling amino and carboxyl terminal
CC   tags, mass spectrometry, circular dichroism to determine conformation or
CC   affinity chromatography columns to purify the protein, cloning or
CC   sequencing. The present sequence is Sistrurus miliarius venom gland
CC   protein, Zsnk4
XX
SQ   Sequence 144 AA;

  Query Match             45.5%;  Score 316.5;  DB 5;  Length 144;
  Best Local Similarity   45.8%;  Pred. No. 1.5e-28;
  Matches   60;  Conservative   24;  Mismatches   38;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :||| | : |:|||:  ||  ||  ||||||||||||||:|:|:  ||:||  ::  |
Db         10 DFDCPSDWYAYDQYCYRVIKQLRTWDDAERFCSEQAKGGHLVSIESDGEAAFVAQLVAEN 69

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVD--PFECFMVSRDTRLREWFKVD 111
                 :     :|||||:| : : |       ||::||||:     :|| : ::|  | |  |
Db         70 IKQNKYDVWIGLRIQGEEKQCSTKWSDGSSVNYENLIKHATKKCFGLKKETGFRTWRNVH 129

Qy        112 CEQQHSFICKF 122
               | ||: |:|||
Db        130 CTQQNLFMCKF 140


RESULT 34
AAE20179
ID   AAE20179 standard; protein; 152 AA.
XX
AC   AAE20179;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Pigmy rattlesnake venom gland protein, Zsnk3.
XX
KW   Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
KW   platelet aggregation; Zsnk3.
XX
OS   Sistrurus miliarius.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT   Protein         24. .152
FT                   /label= Mature_Zsnk3_protein
FT   Disulfide-bond  25. .36
FT   Disulfide-bond  53. .150
FT   Disulfide-bond  125. .142
XX
PN   WO200214364-A2.
XX
PD   21-FEB-2002.
XX
PF   13-AUG-2001; 2001WO-US025310.
XX
```

PR 14-AUG-2000; 2000US-0225072P.
PR 14-AUG-2000; 2000US-0225087P.
PR 15-AUG-2000; 2000US-0225489P.
PR 15-AUG-2000; 2000US-0225490P.
PR 20-DEC-2000; 2000US-0256997P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO, Bishop PD;
XX
DR WPI; 2002-269180/31.
DR N-PSDB; AAD32055.
XX
PT New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which
PT affect blood coagulation and platelet aggregation system, useful in
PT therapy and diagnostics, or as tools in the study of genetics or
PT molecular biology.
XX
PS Claim 3; Page 2; 79pp; English.
XX
CC The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
CC venom gland proteins, which affect blood coagulation and platelet
CC aggregation system. The polypeptides, which affect blood coagulation and
CC platelet aggregation system, are useful in therapy and diagnostics. The
CC polypeptides are also useful as an educational tool in laboratory
CC practical kits for courses related to genetics and molecular biology,
CC protein chemistry and antibody production and analysis. The
CC polynucleotide or polypeptide can be used as standards or as unknowns for
CC testing purposes. The polypeptides are also useful in identifying
CC proteins by western blotting, protein purification, determining the
CC weight of expressed polypeptides as a ratio to total protein expressed,
CC identifying peptide cleavage sites, coupling amino and carboxyl terminal
CC tags, mass spectrometry, circular dichroism to determine conformation or
CC affinity chromatography columns to purify the protein, cloning or
CC sequencing. The present sequence is Sistrurus miliarius venom gland
CC protein, Zsnk3
XX
SQ Sequence 152 AA;

Query Match 45.3%; Score 314.5; DB 5; Length 152;
Best Local Similarity 45.3%; Pred. No. 2.8e-28;
Matches 58; Conservative 25; Mismatches 36; Indels 9; Gaps 2;

```
Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|||||| |::||: ||| || |||||||||:||||:|:|:: ||:||  ::  |:
Db         24 DCPSGWSSYDQHCYRVFKQLKTWDDAERFCSEQAEGGHLVSIESSEEAAFVAQLVPENRR 83

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVDCE 113
                |||||||| | : |       ||:|||| ::     |  : : |   :|  : |
Db         84 RAILYIWIGLRVQGKEKQCSAKWSDGSSVSYENWIEAESKTCLGLQQGTNYHKWVNIYCG 143

Qy        114 QQHSFICK 121
              : : |:|:
Db        144 EINPFVCE 151
```

RESULT 35
AAR45156
ID AAR45156 standard; protein; 133 AA.
XX
AC AAR45156;
XX
DT 25-MAR-2003 (revised)
DT 08-JUN-1994 (first entry)
XX
DE Botrocetin alpha subunit.
XX
KW Botrocetin; alpha subunit; snake venom; Bothrops jararaca;
KW von Willebrand factor; von Willebrand disease.
XX
OS Bothrops jararaca.
XX
PN EP574621-A1.
XX
PD 22-DEC-1993.
XX
PF 02-JUN-1992; 92EP-00305046.
XX
PR 02-JUN-1992; 92EP-00305046.
XX
PA (UYFU-) UNIV FUJITA HEALTH.
PA (GENZ) GENZYME CORP.
XX
PI Titani K, Fujimura Y;
XX
DR WPI; 1993-407054/51.
XX
PT Use of purified botrocetin and opt. ristocetin - for detection of von
PT Willebrand Factor in serum or plasma, for diagnosis of von Willebrand's
PT disease.
XX
PS Disclosure; Page 8; 14pp; English.
XX
CC Botrocetin, isolated from Bothrops jararaca venom, is a disulfide- linked
CC heterodimer comprising an alpha subunit (AAR45156) and a beta subunit
CC (AAR45157). The protein is used to assay von Willebrand factor in serum
CC or plasma, for diagnosis of von Willebrand disease. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 133 AA;

Query Match 44.7%; Score 311; DB 2; Length 133;
Best Local Similarity 45.9%; Pred. No. 6.1e-28;
Matches 61; Conservative 24; Mismatches 38; Indels 10; Gaps 3;

```
Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVET-ALEASFVDNVLYANK 61
              :||||||| :  ||| |:|:| || |||||||||||||:|::  : |  || :::  |
Db          1 DCPSGWSSYEGNCYKFFQQKMNWADAERFCSEQAKGGHLVSIKIYSKEKDFVGDLVTKNI 60

Qy         62 EYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVDC 112
                :    | ||||||:|| : |       ||:||||:|:    :|| : :|      |  : |
Db         61 QSSDLYAWIGLRVENKEKQCSSEWSDGSSVSYENVVERTVKKCFALEKDLGFVLWINLYC 120

Qy        113 EQQHSFICKFTRP 125
                |:: |:||   |
Db        121 AQKNPFVCKSPPP 133
```

RESULT 36
AAR38223
ID AAR38223 standard; protein; 134 AA.
XX
AC AAR38223;
XX
DT 25-MAR-2003 (revised)
DT 01-OCT-1993 (first entry)
XX
DE Sequence of polypeptide chain of alboaggregin A (AL-A).
XX
KW Venom; snake; platelet-binding protein.
XX
OS Trimeresurus albolabris.
XX
PN WO9311151-A1.
XX
PD 10-JUN-1993.
XX
PF 01-DEC-1992; 92WO-US010344.
XX
PR 03-DEC-1991; 91US-00803630.
PR 05-JUN-1992; 92US-00893929.
XX
PA (UTEM) UNIV TEMPLE.
XX
PI Kirby EP, Peng M;
XX

```
DR   WPI; 1993-196991/24.
XX
PT   New platelet-binding proteins obtained from snake venom - inhibit binding
PT   of von Willebrand factor to platelet membrane glycoprotein IB, useful in
PT   therapy, diagnosis and surgery.
XX
PS   Claim 4; Page 46; 74pp; English.
XX
CC   AL-A may be obtd. from snake venom. It has a mol. wt. of about 45 kDa. AL
CC   -A contains two types of polypeptide chains, with mol. wt. of about 18
CC   kDa and about 15 kDa, respectively. Each of these two types of chains is
CC   actually composed of two subtypes. Thus, AL-A comprises four non-
CC   identical polypeptide chains. A possible variation of AAR38224 has been
CC   found, characterised by Asp at posn. three in lieu of Cys. (Updated on 25
CC   -MAR-2003 to correct PN field.)
XX
SQ   Sequence 134 AA;

  Query Match             44.2%;  Score 307.5;  DB 2;  Length 134;
  Best Local Similarity   42.0%;  Pred. No. 1.6e-27;
  Matches   55;  Conservative   26;  Mismatches   41;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  |  |||: |:|||: | :   | |||||::||  |||:|:||  || ||  ::  |
Db          1 DFHCLPGWSAYDQYCYRVFNEPKNWEDAERFCAKQADSGHLVSIETMGEADFVAQLISEN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
               :    |:||||:|||| | |       ||::||||:  :  :|  : :::  |:|  :
Db         61 IQSKEHYVWIGLKVQNKEQQCSSEWSDGSSVTYENLIKLYMRKCGALEQESGFRKWINLG 120

Qy        112 CEQQHSFICKF 122
              | | : |:|||
Db        121 CIQLNPFVCKF 131


RESULT 37
AAO14520
ID   AAO14520 standard; protein; 154 AA.
XX
AC   AAO14520;
XX
DT   29-AUG-2003  (revised)
DT   16-MAY-2002  (first entry)
XX
DE   Korean adder snake venom salmorin A chain protein.
XX
KW   Korean adder; salmorin protein A chain; snake venom;
KW   fibrinogen clotting inhibition; thrombosis; prothrombin binding;
KW   thrombin binding; blood coagulation.
XX
OS   Gloydius halys brevicaudus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT   Protein         24. .154
FT                   /note= "Mature salmorin A chain protein"
XX
PN   WO200214514-A1.
XX
PD   21-FEB-2002.
XX
PF   26-JUL-2001; 2001WO-KR001277.
XX
PR   27-JUL-2000; 2000KR-00043470.
XX
PA   (BIOB-) BIOBUD CO LTD.
XX
PI   Chung K,  Kim D,  Koh Y;
XX
DR   WPI; 2002-241907/29.
DR   N-PSDB; AAL42015.
XX
PT   New salmorin protein derived from venom of Korean adder Agkistrodon halys
PT   brevicaudus, useful for treating thrombosis by repressing fibrinogen
PT   clotting through repression of activation of prothrombin into thrombin.
XX
PS   Claim 2; Fig 1A; 30pp; English.
XX
CC   The invention comprises the nucleotide and protein sequences of a
CC   salmorin protein derived from the venom of Korean adder. Salmorin protein
CC   is composed of an A chain and a B chain, and has inhibitory activity
CC   against fibrinogen clotting. The salmorin protein of the invention is
CC   useful for treating thrombosis, as it represses fibrinogen clotting
CC   potently by binding to prothrombin and thrombin so as to delay blood
CC   coagulation. The present amino acid sequence represents the Korean adder
CC   salmorin A chain protein. (Updated on 29-AUG-2003 to standardise OS
CC   field)
XX
SQ   Sequence 154 AA;

  Query Match             43.8%;  Score 304.5;  DB 5;  Length 154;
  Best Local Similarity   44.6%;  Pred. No. 4.3e-27;
  Matches   58;  Conservative   20;  Mismatches   43;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  ||||| | : :||: | | |||  |||||| |||||||:|:||  || || :|:
Db         24 DFFCPSGWGSNNGHCYQAFNQRMTWEDAERFCSAQAKGGHLVSIETRAEADFVAHVVAER 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVD 111
               |    ::||||| : | | |       ||:|||| ::     |  :  |:   :|  |
Db         84 IETSFPHVWIGLRDEGKEQQCSSEWSDGSSVSYENWIEAESKTCLGLELDSNYHKWVNVY 143

Qy        112 CEQQHSFICK 121
              | |:: |:|:
Db        144 CGQRNPFVCE 153


RESULT 38
AAM51543
ID   AAM51543 standard; protein; 152 AA.
XX
AC   AAM51543;
XX
DT   11-SEP-2003  (revised)
DT   10-JAN-2002  (first entry)
XX
DE   Snake venom blood anticoagulant halyxin A chain.
XX
KW   Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
KW   thrombosis.
XX
OS   Gloydius halys.
XX
PN   KR2001049671-A.
XX
PD   15-JUN-2001.
XX
PF   29-JUN-2000; 2000KR-00036591.
XX
PR   29-JUN-1999;   99KR-00025105.
XX
PA   (BIOB-) BIOBUD CO LTD.
XX
PI   Jang YS,  Jung GH,  Kim DS,  Koo BH,  Son YD;
XX
DR   WPI; 2001-637330/73.
DR   N-PSDB; AAI71876.
XX
PT   Halyxin as blood anticoagulation protein separated from snake venom.
XX
PS   Claim 2; Page 10; 21pp; Korean.
XX
CC   The invention relates to halyxin, a novel protein with very strong blood
CC   anticoagulation activity. The protein was separated from snake venom of
CC   Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the
```

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CC   treatment of thrombogenesis. The present sequence is the A chain of
CC   halyxin. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 152 AA;

  Query Match             42.1%;  Score 292.5;  DB 4;  Length 152;
  Best Local Similarity   41.4%;  Pred. No. 1.1e-25;
  Matches   53;  Conservative   27;  Mismatches   39;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||||||| : :||  |    ||| ||||| :| || ||:|:|:: || ||  ::  | :
Db         24 DCPSGWSSYEGHCYNIFHLFKTWAEAERFCRKQVKGAHLVSIESSEEADFVAQLVSENMK 83

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVDCE 113
                ||||||||: | : |       ||:||:| ::     |  : ::|  |:|| : |
Db         84 RYGIYIWIGLRVRGKKKQCSSQWSDGSSVSYQNWIEAESKTCLGLQKETEFRKWFNIYCG 143

Qy        114 QQHSFICK 121
              ::: |:|:
Db        144 ERNPFVCE 151


RESULT 39
ABB79130
ID   ABB79130 standard; protein; 132 AA.
XX
AC   ABB79130;
XX
DT   06-AUG-2002  (first entry)
XX
DE   Ahylysantinfarctase thrombase I subunit A SEQ ID NO:1.
XX
KW   Ahylysantinfarctase thrombase I; Chinese Agkistrodon acutus; snake venom;
KW   enzyme; Deinagkistrodon acutus.
XX
OS   Deinagkistrodon acutus.
XX
PN   CN1332241-A.
XX
PD   23-JAN-2002.
XX
PF   29-APR-2001; 2001CN-00115567.
XX
PR   29-APR-2001; 2001CN-00115567.
XX
PA   (KUNM-) KUNMING ZOOLOGY INST CHINESE ACAD SCI.
XX
PI   Xiao C;
XX
DR   WPI; 2002-281832/33.
XX
PT   Ahylysantinfarctase thrombase and its production process.
XX
PS   Claim 4; Page 5 (Disclosure); 8pp; Chinese.
XX
CC   The present sequence represents subunit A of the ahylysantinfarctase
CC   thrombase I isolated from the snake venom of Chinese Agkistrodon acutus
CC   (Deinagkistrodon acutus). The present invention describes an anionic
CC   exchange column chromatographic process used to separate and purify, and
CC   the repurifying in a fast protein purifying work station, where
CC   Ahylysantinfarctase thrombase I of over 97% purity is obtained from snake
CC   venom of Chinese Agkistrodon acutus. The test shows that the
CC   Ahylysantinfarctase thrombase I consists of two subunits designated A and
CC   B (see ABB79130 and ABB79131 respectively)
XX
SQ   Sequence 132 AA;

  Query Match             39.4%;  Score 274;  DB 5;  Length 132;
  Best Local Similarity   39.7%;  Pred. No. 1.3e-23;
  Matches   52;  Conservative   28;  Mismatches   39;  Indels   12;  Gaps    4;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  || |||: | :||   |:   |  ||:||:||| ||||:|:|:  |  |:  ::  :
Db          1 DFNCPPGWSAYD-HCY--IKEPKNWDDAEKFCTEQADGGHLVSIESKGERDFLAQLVSQS 57

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
                | :  ::| |||:||| : |       ||:|:|||:: :  :|  : |||   :|  :
Db         58 IESIEDHVWTGLRLQNKEKQCSTEWSDGSSLSFENLLELYMRKCGALDRDTGFHKWINLG 117

Qy        112 CEQQHSFICKF 122
              | | : |:|||
Db        118 CIQLNPFVCKF 128


RESULT 40
ABU08798
ID   ABU08798 standard; protein; 129 AA.
XX
AC   ABU08798;
XX
DT   02-JUN-2003  (first entry)
XX
DE   Deinagkistrodon acutus antithrombosis enzyme alpha chain.
XX
KW   Antithrombosis; alpha chain; fibrin hydrolysis; blood clot; enzyme;
KW   platelet aggregation; vaso-occulusive disorder; thromboembolic disorder;
KW   myocardial infarction; restenosis; cancer; neurodegenerative disease;
KW   angiopathic thrombosis; cerebral thrombosis; thromboangiitis obliterans;
KW   ischaemic cerebral vascular disease; unstable angina; acute thrombosis;
KW   unstable stenocardia; pulmonary embolism; deep vein thrombosis; oedema;
KW   peripheral arterial occulsion; stroke; atherosclerosis; inflammation;
KW   thrombosis.
XX
OS   Deinagkistrodon acutus.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .29
FT                   /note= "Specifically claimed in claim 7"
FT   Region          1. .9
FT                   /note= "Antithrombosis enzyme alpha chain N-terminus not
FT                   encoded by abx93668"
FT   Misc-difference 91
FT                   /note= "Encoded by TAT"
XX
PN   US6489451-B1.
XX
PD   03-DEC-2002.
XX
PF   10-APR-1998;   98US-00058740.
XX
PR   10-APR-1997;   97US-0043886P.
XX
PA   (HEFE-) HEFEI SIU FUNG USTC PHARM CO LTD.
XX
PI   Li BX,  Cheng X;
XX
DR   WPI; 2003-352116/33.
DR   N-PSDB; ABX93668.
XX
PT   New purified Agkistrodon actus anti-thrombosis enzyme, useful for
PT   preventing and treating vaso-occulusive and thromboembolic disorders,
PT   including myocardial infarction, restenosis, cerebral thrombosis and
PT   unstable angina.
XX
PS   Claim 12; Col 11; 19pp; English.
XX
CC   The invention relates to a new Deinagkistrodon actus anti-thrombosis
CC   enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and
CC   prevents platelet aggregation. The anti-thrombosis enzyme was
CC   administered to rabbits intravenously. Thrombosis was determined before
CC   and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the
CC   Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour
CC   following administration at 0.005 micro/kg and this activity was
CC   increased significantly at 1.0 hour and at 0.01 micro /kg. The
CC   composition is useful for preventing and treating vaso-occulusive and
CC   thromboembolic disorders, including myocardial infarction, restenosis,
```

```
CC   angiopathic thrombosis, cerebral thrombosis, ischaemic cerebral vascular
CC   diseases, unstable angina, acute thrombosis, unstable stenocardia,
CC   thromboangiitis obliterans, pulmonary embolism, deep vein thrombosis,
CC   peripheral arterial occulsion, stroke. It is also useful for treating
CC   atherosclerosis, oedema and inflammation, cancer and neurodegenerative
CC   diseases. The present sequence represents the amino acid sequence of the
CC   Deinagkistrodon acutus antithrombosis enzyme alpha chain
XX
SQ   Sequence 129 AA;

  Query Match             39.1%;  Score 271.5;  DB 6;  Length 129;
  Best Local Similarity   41.4%;  Pred. No. 2.4e-23;
  Matches   53;  Conservative   22;  Mismatches   44;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :| | ||| : :||| |||  ||  || ||::|  ||||:|:|:: || ||  ::    :
Db          1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                ::||||| ||| : |       |||| || :  :  :|  |  :|   :|    ||
Db         61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120

Qy        114 QQHSFICK 121
                 || .|:|:
Db        121 QQDPFVCE 128


RESULT 41
ABU62534
ID   ABU62534 standard; protein; 129 AA.
XX
AC   ABU62534;
XX
DT   23-OCT-2003  (revised)
DT   29-AUG-2003  (first entry)
XX
DE   Snake antithrombosis enzyme A chain.
XX
KW   Snake; antithrombosis enzyme; A chain; enzyme; fibrin; blood clot;
KW   platelet aggregation; myocardial infarction; restenosis; unstable angina;
KW   cerebral thrombosis; cardiant; antianginal; thrombolytic; anticoagulant;
KW   vasotropic.
XX
OS   Deinagkistrodon acutus.
XX
PN   US2003022350-A1.
XX
PD   30-JAN-2003.
XX
PF   23-AUG-2001; 2001US-00938114.
XX
PR   11-APR-1997;   97US-0043886P.
PR   10-APR-1998;   98US-00058740.
XX
PA   (WANG/) WANG C.
PA   (LIBX/) LI B X.
PA   (CHEN/) CHENG X.
PA   (LIUJ/) LIU J.
PA   (NIUL/) NIU L.
PA   (HUAN/) HUANG W.
PA   (XUZZ/) XU Z.
PA   (LUOD/) LUO D.
PA   (KANG/) KANG L.
PA   (DING/) DING J.
PA   (RONG/) RONG F.
PA   (LIUY/) LIU Y.
PA   (CHEN/) CHEN H.
XX
PI   Wang C,  Li BX,  Cheng X,  Liu J,  Niu L,  Huang W,  Xu Z,  Luo D;
PI   Kang L,  Ding J,  Rong F,  Liu Y,  Chen H;
XX
DR   WPI; 2003-492002/46.
XX
PT   New antithrombosis enzyme, useful for treating or preventing a thrombosis
PT   related disease in a mammal e.g. myocardial infarction, restenosis,
PT   unstable angina or cerebral thrombosis.
XX
PS   Claim 14; Page 6-7; 20pp; English.
XX
CC   The invention relates to an isolated, purified or recombinant
CC   antithrombosis enzyme which hydrolyses fibrin, dissolves blood clots and
CC   prevents platelet aggregation. The enzyme is useful for treating or
CC   preventing a thrombosis related disease in a mammal, such as myocardial
CC   infarction, restenosis, unstable angina or cerebral thrombosis. This
CC   sequence represents a snake antithrombosis enzyme A chain. (Updated on 23
CC   -OCT-2003 to standardise OS field)
XX
SQ   Sequence 129 AA;

  Query Match             39.1%;  Score 271.5;  DB 7;  Length 129;
  Best Local Similarity   41.4%;  Pred. No. 2.4e-23;
  Matches   53;  Conservative   22;  Mismatches   44;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :| | ||| : :||| |||  ||  || ||::|  ||||:|:|:: || ||  ::    :
Db          1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                ::||||| ||| : |       |||| || :  :  :|  |  :|   :|    ||
Db         61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120

Qy        114 QQHSFICK 121
                 || .|:|:
Db        121 QQDPFVCE 128


RESULT 42
AAR72235
ID   AAR72235 standard; peptide; 132 AA.
XX
AC   AAR72235;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   04-DEC-1995  (first entry)
XX
DE   Vipera palestinae venom derived peptide.
XX
KW   Vipera palestinae; venom; antithrombotic agent; platelet binding;
KW   von Willebrand factor.
XX
OS   Vipera xanthina.
XX
PN   WO9509183-A1.
XX
PD   06-APR-1995.
XX
PF   27-SEP-1994;   94WO-JP001583.
XX
PR   28-SEP-1993;   93JP-00241666.
PR   14-JAN-1994;   94JP-00002691.
PR   10-JUN-1994;   94JP-00128518.
XX
PA   (AJIN ) AJINOMOTO KK.
XX
PI   Fukuchi N,  Ishii K,  Kaida K,  Kobayashi T;
XX
DR   WPI; 1995-147392/19.
XX
PT   Peptide derived from Vipera palestinae venom - inhibits binding of
PT   platelets to von Willebrand factor, useful as antithrombotic agent.
XX
PS   Claim 5; Page 19; 37pp; Japanese.
XX
CC   AAR72235 is a Vipera palestinae venom derived peptide. A peptide compsn.
CC   comprising AAR72235 and AAR72236 is claimed, it inhibits the binding of
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CC   platelets to von Willebrand factors and can therefore be used as an anti-
CC   thrombotic agent. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 132 AA;

  Query Match             37.8%;  Score 262.5;  DB 2;  Length 132;
  Best Local Similarity   39.8%;  Pred. No. 2.8e-22;
  Matches   51;  Conservative   22;  Mismatches   48;  Indels    7;  Gaps    1;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :||| ||| : :||| |:   ||  ||:|| :|  | || |:|:  ||:||  ::
Db          1 DQDCPSDWSSHEGHCYKVFRLFKTWEEAEKFCMQQVNGWHLASIESVEEANFVAELVSKT 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSS-------ISYENLVDPFECFMVSRDTRLREWFKVDCE 113
                 : ||||| |:: | |||       :||| :    :|| :::|    ||  : ||
Db         61 LIKSKYHAWIGLRDQSERQQCSSHWTDGSAVSYETVTKYTKCFGLNKDKGYLEWVTLPCE 120

Qy        114 QQHSFICK 121
               :  ||||
Db        121 DKIPFICK 128


RESULT 43
AAR38230
ID   AAR38230 standard; protein; 133 AA.
XX
AC   AAR38230;
XX
DT   25-MAR-2003  (revised)
DT   01-OCT-1993  (first entry)
XX
DE   Sequence of polypeptide chain of alboaggregin-like protein called
DE   echicetin.
XX
KW   Venom; snake; platelet-binding protein.
XX
OS   Echis carinatus.
XX
PN   WO9311151-A1.
XX
PD   10-JUN-1993.
XX
PF   01-DEC-1992;   92WO-US010344.
XX
PR   03-DEC-1991;   91US-00803630.
PR   05-JUN-1992;   92US-00893929.
XX
PA   (UTEM ) UNIV TEMPLE.
XX
PI   Kirby EP,  Peng M;
XX
DR   WPI; 1993-196991/24.
XX
PT   New platelet-binding proteins obtained from snake venom - inhibit binding
PT   of von Willebrand factor to platelet membrane glycoprotein IB, useful in
PT   therapy, diagnosis and surgery.
XX
PS   Claim 10; Page 49; 74pp; English.
XX
CC   Echicetin, is obtained in substantially pure chemical for from venom, as
CC   an about 26 kDa protein which likely comprises a dimer composed of two
CC   types of chains. One chain type has a mol. wt. of about 15 kDa and the
CC   other has a mol. wt. of about 13 kDa. The individual polypeptide chains
CC   are held together by one or more interchain disulfide bonds. (Updated on
CC   25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 133 AA;

  Query Match             36.9%;  Score 256.5;  DB 2;  Length 133;
  Best Local Similarity   37.8%;  Pred. No. 1.4e-21;
  Matches   51;  Conservative   30;  Mismatches   43;  Indels   11;  Gaps    4;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :| ||||  : :||: |: : ||  ||::|: |  ||||:|:|:  :| ||  ::
Db          1 DQDCLSGWSFYEGHCYQLFRLK-TWDEAEKYCN-QWDGGHLVSIESNAKAEFVAQLISRK 58

Qy         61 --KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKVD 111
                |  :   :|||| ::| : |       | : ||::| | :||:: | |  |:|  |:
Db         59 LPKSAIEDRVWIGLRDRSKREQCGHLWTDNSFVHYEHVVPPTKCFVLERQTEFRKWIAVN 118

Qy        112 CEQQHSFICKFTRPR 126
              || :  |:||   ||
Db        119 CEFKFPFVCKAKIPR 133


RESULT 44
AAR38225
ID   AAR38225 standard; protein; 123 AA.
XX
AC   AAR38225;
XX
DT   25-MAR-2003  (revised)
DT   01-OCT-1993  (first entry)
XX
DE   Sequence of polypeptide chain of alboaggregin A (AL-A).
XX
KW   Venom; snake; platelet-binding protein.
XX
OS   Trimeresurus albolabris.
XX
PN   WO9311151-A1.
XX
PD   10-JUN-1993.
XX
PF   01-DEC-1992;   92WO-US010344.
XX
PR   03-DEC-1991;   91US-00803630.
PR   05-JUN-1992;   92US-00893929.
XX
PA   (UTEM ) UNIV TEMPLE.
XX
PI   Kirby EP,  Peng M;
XX
DR   WPI; 1993-196991/24.
XX
PT   New platelet-binding proteins obtained from snake venom - inhibit binding
PT   of von Willebrand factor to platelet membrane glycoprotein IB, useful in
PT   therapy, diagnosis and surgery.
XX
PS   Claim 4; Page 47; 74pp; English.
XX
CC   AL-A may be obtd. from snake venom. It has a mol. wt. of about 45 kDa. AL
CC   -A contains two types of polypeptide chains, with mol. wt. of about 18
CC   kDa and about 15 kDa, respectively. Each of these two types of chains is
CC   actually composed of two subtypes. Thus, AL-A comprises four non-
CC   identical polypeptide chains. A possible variation of AAR38224 has been
CC   found, characterised by Asp at posn. three in lieu of Cys. (Updated on 25
CC   -MAR-2003 to correct PN field.)
XX
SQ   Sequence 123 AA;

  Query Match             35.0%;  Score 243.5;  DB 2;  Length 123;
  Best Local Similarity   38.9%;  Pred. No. 4.3e-20;
  Matches   51;  Conservative   22;  Mismatches   37;  Indels   21;  Gaps    6;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDN----VLY 58
              :||| ||| : :||: | :   || ||:||::| || ||:| :::   | ||      :|
Db          1 DCPSDWSSYEGHCYRVFNEPQNWADAEKFCTQQHKGSHLVSFQSSGGADFVVQMTRPILN 60

Qy         59 ANKEYLTRYIWIGLRVQNKGQPCSS-------ISYENLVDPFECFMVSRDTRLREWFKVD 111
              ||      :||||   |     |:|       : |:   : ||| :||| |    ||  :|
Db         61 AN------LVWIGL--SNLWNGCNSQWSDGTXLDYKXWREQFEC-LVSRTTN-NEWLSMD 110

Qy        112 CEQQHSFICKF 122
              |   |||:|:|
```

```
Db        111 CSSTHSFVCEF 121


RESULT 45
AAR72236
ID   AAR72236 standard; peptide; 127 AA.
XX
AC   AAR72236;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   04-DEC-1995  (first entry)
XX
DE   Vipera palestinae venom derived peptide.
XX
KW   Vipera palestinae; venom; antithrombotic agent; platelet binding;
KW   von Willebrand factor.
XX
OS   Vipera xanthina.
XX
PN   WO9509183-A1.
XX
PD   06-APR-1995.
XX
PF   27-SEP-1994;   94WO-JP001583.
XX
PR   28-SEP-1993;   93JP-00241666.
PR   14-JAN-1994;   94JP-00002691.
PR   10-JUN-1994;   94JP-00128518.
XX
PA   (AJIN ) AJINOMOTO KK.
XX
PI   Fukuchi N,  Ishii K,  Kaida K,  Kobayashi T;
XX
DR   WPI; 1995-147392/19.
XX
PT   Peptide derived from Vipera palestinae venom - inhibits binding of
PT   platelets to von Willebrand factor, useful as antithrombotic agent.
XX
PS   Claim 5; Page 19-20; 37pp; Japanese.
XX
CC   AAR72236 is a Vipera palestinae venom derived peptide. A peptide compsn.
CC   comprising AAR72235 and AAR72236 is claimed, it inhibits the binding of
CC   platelets to von Willebrand factors and can therefore be used as an anti-
CC   thrombotic agent. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC   on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 127 AA;

  Query Match             32.6%;  Score 226.5;  DB 2;  Length 127;
  Best Local Similarity   36.6%;  Pred. No. 4.3e-18;
  Matches   48;  Conservative   23;  Mismatches   47;  Indels   13;  Gaps    4;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| : :||| |  : ||| ||:||:|| ||||||::: |  |:  :::   :
Db          1 DCPSDWSSHEGHCYKVFNLDKTWADAEKFCTEQVSGGHLLSLKSTEEVDFMIKLVFPILK 60

Qy         63 YLTRYIWIGLRVQNKGQPCS-------SISYENLVDPFECFMVSRDTRLREWFKVDCEQQ 115
              |    |||||    |  : |         : |:   |  :|::    |   :|   || :
Db         61 Y--DLIWIGL--SNFWRDCHWGWSDGVKLDYKAWSDIPDCYVAK--TVDYQWLLRDCSRT 114

Qy        116 HSFICKFTRPR 126
              : ||||   ||
Db        115 YKFICKSRVPR 125


RESULT 46
AAM51544
ID   AAM51544 standard; protein; 146 AA.
XX
AC   AAM51544;
XX
DT   11-SEP-2003  (revised)
DT   10-JAN-2002  (first entry)
XX
DE   Snake venom blood anticoagulant halyxin B chain.
XX
KW   Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
KW   thrombosis.
XX
OS   Gloydius halys.
XX
PN   KR2001049671-A.
XX
PD   15-JUN-2001.
XX
PF   29-JUN-2000; 2000KR-00036591.
XX
PR   29-JUN-1999;   99KR-00025105.
XX
PA   (BIOB-) BIOBUD CO LTD.
XX
PI   Jang YS,  Jung GH,  Kim DS,  Koo BH,  Son YD;
XX
DR   WPI; 2001-637330/73.
DR   N-PSDB; AAI71877.
XX
PT   Halyxin as blood anticoagulation protein separated from snake venom.
XX
PS   Claim 2; Page 11-12; 21pp; Korean.
XX
CC   The invention relates to halyxin, a novel protein with very strong blood
CC   anticoagulation activity. The protein was separated from snake venom of
CC   Agkistrodon halys brevicaudus (a Korean pit viper) and can be used in the
CC   treatment of thrombogenesis. The present sequence is the B chain of
CC   halyxin. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 146 AA;

  Query Match             30.3%;  Score 210.5;  DB 4;  Length 146;
  Best Local Similarity   34.6%;  Pred. No. 3.8e-16;
  Matches   44;  Conservative   21;  Mismatches   49;  Indels   13;  Gaps    4;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||||||| : :||||| ::  || || ||::|  ||||:|  :  || ||  : : |
Db         24 DCPSGWSSYEGHCYKPFNEQKNWADAENFCTQQHTGGHLVSFHSTEEADFVVKLAFQN-- 81

Qy         63 YLTRYIWIGLRVQNKGQPCS-------SISYENLVDPFECFMVSRDTRLREWFKVDCEQQ 115
              :     |:||   |    ||         : ||   :  | : |   :   :|    | :
Db         82 FGHGIFWMGL--SNVWNQCSWQWSSAAKLKYEAWAE--ESYCVYFKSTNNKWRSRACRME 137

Qy        116 HSFICKF 122
              |:|:|
Db        138 AYFVCEF 144


RESULT 47
ABU08799
ID   ABU08799 standard; protein; 146 AA.
XX
AC   ABU08799;
XX
DT   02-JUN-2003  (first entry)
XX
DE   Deinagkistrodon acutus antithrombosis enzyme beta chain.
XX
KW   Antithrombosis; beta chain; fibrin hydrolysis; blood clot; enzyme;
KW   platelet aggregation; vaso-occulusive disorder; thromboembolic disorder;
KW   myocardial infarction; restenosis; cancer; neurodegenerative disease;
KW   angiopathic thrombosis; cerebral thrombosis; thromboangiitis obliterans;
KW   ischaemic cerebral vascular disease; unstable angina; acute thrombosis;
KW   unstable stenocardia; pulmonary embolism; deep vein thrombosis; oedema;
KW   peripheral arterial occulsion; stroke; atherosclerosis; inflammation;
KW   thrombosis.
XX
OS   Deinagkistrodon acutus.
```

```
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /note= "Leader peptide"
FT   Protein         24. .146
FT                   /note= "Mature antithrombosis enzyme beta chain. Residues
FT                   24 to 40 specifically claimed in claim 8"
FT   Misc-difference 72
FT                   /label= Unknown
FT                   /note= "Encoded by NNT"
FT   Misc-difference 72
FT                   /label= Unknown
FT                   /note= "Encoded by NNN"
FT   Misc-difference 72
FT                   /label= Unknown
FT                   /note= "Encoded by NNN"
FT   Misc-difference 72
FT                   /label= Unknown
FT                   /note= "Encoded by TNN"
XX
PN   US6489451-B1.
XX
PD   03-DEC-2002.
XX
PF   10-APR-1998;   98US-00058740.
XX
PR   10-APR-1997;   97US-0043886P.
XX
PA   (HEFE-) HEFEI SIU FUNG USTC PHARM CO LTD.
XX
PI   Li BX,  Cheng X;
XX
DR   WPI; 2003-352116/33.
DR   N-PSDB; ABX93674.
XX
PT   New purified Agkistrodon actus anti-thrombosis enzyme, useful for
PT   preventing and treating vaso-occulusive and thromboembolic disorders,
PT   including myocardial infarction, restenosis, cerebral thrombosis and
PT   unstable angina.
XX
PS   Disclosure; Fig 1; 19pp; English.
XX
CC   The invention relates to a new Deinagkistrodon actus anti-thrombosis
CC   enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and
CC   prevents platelet aggregation. The anti-thrombosis enzyme was
CC   administered to rabbits intravenously. Thrombosis was determined before
CC   and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the
CC   Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour
CC   following administration at 0.005 micro/kg and this activity was
CC   increased significantly at 1.0 hour and at 0.01 micro /kg. The
CC   composition is useful for preventing and treating vaso-occulusive and
CC   thromboembolic disorders, including myocardial infarction, restenosis,
CC   angiopathic thrombosis, cerebral thrombosis, ischaemic cerebral vascular
CC   diseases, unstable angina, acute thrombosis, unstable stenocardia,
CC   thromboangiitis obliterans, pulmonary embolism, deep vein thrombosis,
CC   peripheral arterial occulsion, stroke. It is also useful for treating
CC   atherosclerosis, oedema and inflammation, cancer and neurodegenerative
CC   diseases. The present sequence represents the amino acid sequence of the
CC   Deinagkistrodon acutus antithrombosis enzyme beta chain
XX
SQ   Sequence 146 AA;

  Query Match             30.3%;  Score 210.5;  DB 6;  Length 146;
  Best Local Similarity   37.6%;  Pred. No. 3.8e-16;
  Matches   47;  Conservative   23;  Mismatches   46;  Indels    9;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHL-LSVETALEASFVDNVLYANK 61
              :||| ||| : :||||| :  ||| ||:||::| || || |:   |:      :| :
Db         24 DCPSEWSSYEGHCYKPFDEPKTWADAEKFCTQQHKGSHLPLTAVRAIVXXXXGHVDHTKL 83

Qy         62 EYLT----RYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHS 117
              : ::    : || |      |    : : |::  : ||| :||| |   ||  :||    |
Db         84 KLISLIGLKNIWNG--CYWKWSDGTKLDYKDWREQFEC-LVSR-TVNNEWLSMDCGTTCS 139

Qy        118 FICKF 122
              |:|||
Db        140 FVCKF 144


RESULT 48
ABU62539
ID   ABU62539 standard; protein; 146 AA.
XX
AC   ABU62539;
XX
DT   23-OCT-2003  (revised)
DT   29-AUG-2003  (first entry)
XX
DE   Snake antithrombosis enzyme B chain.
XX
KW   Snake; antithrombosis enzyme; B chain; enzyme; fibrin; blood clot;
KW   platelet aggregation; myocardial infarction; restenosis; unstable angina;
KW   cerebral thrombosis; cardiant; antianginal; thrombolytic; anticoagulant;
KW   vasotropic.
XX
OS   Deinagkistrodon acutus.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 72. .75
FT                   /note= "Encoded by TNNNNNNNNNNT"
XX
PN   US2003022350-A1.
XX
PD   30-JAN-2003.
XX
PF   23-AUG-2001; 2001US-00938114.
XX
PR   11-APR-1997;   97US-0043886P.
PR   10-APR-1998;   98US-00058740.
XX
PA   (WANG/) WANG C.
PA   (LIBX/) LI B X.
PA   (CHEN/) CHENG X.
PA   (LIUJ/) LIU J.
PA   (NIUL/) NIU L.
PA   (HUAN/) HUANG W.
PA   (XUZZ/) XU Z.
PA   (LUOD/) LUO D.
PA   (KANG/) KANG L.
PA   (DING/) DING J.
PA   (RONG/) RONG F.
PA   (LIUY/) LIU Y.
PA   (CHEN/) CHEN H.
XX
PI   Wang C,  Li BX,  Cheng X,  Liu J,  Niu L,  Huang W,  Xu Z,  Luo D;
PI   Kang L,  Ding J,  Rong F,  Liu Y,  Chen H;
XX
DR   WPI; 2003-492002/46.
DR   N-PSDB; ACA63110.
XX
PT   New antithrombosis enzyme, useful for treating or preventing a thrombosis
PT   related disease in a mammal e.g. myocardial infarction, restenosis,
PT   unstable angina or cerebral thrombosis.
XX
PS   Example 3; Fig 1; 20pp; English.
XX
CC   The invention relates to an isolated, purified or recombinant
CC   antithrombosis enzyme which hydrolyses fibrin, dissolves blood clots and
CC   prevents platelet aggregation. The enzyme is useful for treating or
CC   preventing a thrombosis related disease in a mammal, such as myocardial
CC   infarction, restenosis, unstable angina or cerebral thrombosis. This
CC   sequence represents a snake antithrombosis enzyme B chain. (Updated on 23
CC   -OCT-2003 to standardise OS field)
XX
SQ   Sequence 146 AA;
```

```
  Query Match            30.3%;  Score 210.5;  DB 7;  Length 146;
  Best Local Similarity  37.6%;  Pred. No. 3.8e-16;
  Matches   47;  Conservative   23;  Mismatches   46;  Indels    9;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHL-LSVETALEASFVDNVLYANK 61
              :||| ||| : :||||| :  ||| ||:||::| || || |:   |:      :| :
Db         24 DCPSEWSSYEGHCYKPFDEPKTWADAEKFCTQQHKGSHLPLTAVRAIVXXXXGHVDHTKL 83

Qy         62 EYLT----RYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHS 117
              : ::    : || |     |    : : |::  : ||| :||| |   || :||    |
Db         84 KLISLIGLKNIWNG--CYWKWSDGTKLDYKDWREQFEC-LVSR-TVNNEWLSMDCGTTCS 139

Qy        118 FICKF 122
              |:|||
Db        140 FVCKF 144


RESULT 49
AAR24427
ID   AAR24427 standard; protein; 116 AA.
XX
AC   AAR24427;
XX
DT   25-MAR-2003  (revised)
DT   21-NOV-1992  (first entry)
XX
DE   Sequence of the platelet glycoprotein GPIb inhibitor beta chain (CHH-B-
DE   beta).
XX
KW   Platelet adherence inhibitor; platelet anti-adhesive;
KW   antithrombotic agent; von Willebrand Factor;
KW   platelet glycoprotein GPIb-IX complex.
XX
OS   Crotalus horridus horridus.
XX
PN   WO9208472-A1.
XX
PD   29-MAY-1992.
XX
PF   14-NOV-1991;   91WO-US008516.
XX
PR   16-NOV-1990;   90US-00614443.
XX
PA   (CORT-) COR THERAPEUTICS INC.
XX
PI   Scarborough RM;
XX
DR   WPI; 1992-199936/24.
XX
PT   Platelet antiadhesive peptide(s) obtd. from snake venom - also inhibit
PT   thrombus formation; for treatment of arteriosclerosis, atherosclerosis,
PT   acute myocardial infarction, chronic unstable angina, etc.
XX
PS   Example; Fig 6; 5pp; English.
XX
CC   The PAA was purified from a solution of snake venom. Analysis of the peak
CC   inhibitory fractions by SDS-PAGE revealed 2 major proteins migrating with
CC   a mol. wt. 23-28 kD. Both were able to inhibit botrocetin and ristocetin
CC   induced platelet agglutination. They were called CHH-A and CHH-B. The
CC   earlier eluting subunit (CHH-B-beta) and later eluting subunit (CHH-B-
CC   alpha) were individually submitted to N-terminal sequence analysis. The
CC   complete amino acid sequence for the alpha and beta chains are given in
CC   AAR24426 and AAR24427. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 116 AA;

  Query Match            30.1%;  Score 209;  DB 2;  Length 116;
  Best Local Similarity  37.1%;  Pred. No. 4.2e-16;
  Matches   46;  Conservative   26;  Mismatches   40;  Indels   12;  Gaps    6;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| : :||: |:|||||  ||:||::|  ||||:|  :: |  |: ::|   |:
Db          1 DCPSDWSSYEGHCYRVFQQEMTWDDAEKFCTQQHTGGHLVSFRSSEEVDFLVSIL---KD 57

Qy         63 YL---TRYIWIGLRVQ-NKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSF 118
                 | ||   |:| : |   : ::|:      || :| | |   :|    | : |:
Db         58 LFWMGWRDIWNERRLQWSDG---TKVNYKAWSAEPEC-IVCRATD-NQWLSTSCSKTHNV 112

Qy        119 ICKF 122
              :|||
Db        113 VCKF 116


RESULT 50
AAR71978
ID   AAR71978 standard; peptide; 38 AA.
XX
AC   AAR71978;
XX
DT   25-MAR-2003  (revised)
DT   28-NOV-1995  (first entry)
XX
DE   Snake venom derived antithrombotic peptide.
XX
KW   Antithrombotic peptide; snake venom; platelet binding inhibition;
KW   von Willebrand factors; Crotalus horridus horridus.
XX
OS   Crotalus horridus horridus.
XX
FH   Key             Location/Qualifiers
FT   Disulfide-bond  4. .15
XX
PN   WO9508573-A1.
XX
PD   30-MAR-1995.
XX
PF   21-SEP-1994;   94WO-JP001555.
XX
PR   22-SEP-1993;   93JP-00236975.
XX
PA   (AJIN ) AJINOMOTO KK.
XX
PI   Fukuchi N,  Yamamoto H,  Nagano M,  Kito M,  Tanaka A,  Ishii K;
PI   Kobayashi T,  Yoshimoto R;
XX
DR   WPI; 1995-139559/18.
XX
PT   Single-chain antithrombotic peptide - obtained by cleaving an
PT   oligopeptide from snake venom to break inter-chain di:sulphide bonds but
PT   preserve intra-chain di:sulphide bonds.
XX
PS   Claim 3; Page 44; 84pp; Japanese.
XX
CC   AAR71978 and AAR71979 are snake venom derived antithrombotic peptides,
CC   prepared by cleaving the interpeptide but retaining the intrapeptide
CC   disulphide bonds of the original snake venom oligopeptide. These peptides
CC   have the advantage of avoiding significant thrombocytopenia when
CC   administered at the minimun dose, for in vivo inhibition of platelet von
CC   Willebrand factor binding. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 38 AA;

  Query Match            29.9%;  Score 208;  DB 2;  Length 38;
  Best Local Similarity  94.7%;  Pred. No. 1.3e-16;
  Matches   36;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKG 38
              |||||||||| |||||||||||||| ||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKG 38


Search completed: May  2, 2005, 16:00:34
Job time : 77 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 2, 2005, 15:59:06 ; Search time 20 Seconds
(without alignments)
606.166 Million cell updates/sec

Title: US-10-749-387-1
Perfect score: 695
Sequence: 1 DLECPSGWSSTDRYCYKPFK.....WFKVDCEQQHSFICKFTRPR 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	332.5	47.8	129	2	JC4329	coagulation factor
2	311	44.7	133	2	A47267	botrocetin alpha c
3	302.5	43.5	152	2	JC4690	coagulation factor
4	291.5	41.9	152	2	JC7134	agkisacutacin alph
5	288	41.4	144	2	PC7027	aggretin alpha cha
6	248.5	35.8	146	2	JC7135	agkisacutacin beta
7	242.5	34.9	131	2	JC5058	bitiscetin alpha c
8	225.5	32.4	146	2	JC7105	aggretin beta chai
9	218.5	31.4	123	2	B42972	coagulation factor
10	196.5	28.3	125	2	JC5059	bitiscetin beta ch
11	192.5	27.7	146	2	JC4691	coagulation factor
12	191.5	27.6	125	2	B47267	botrocetin beta ch
13	179.5	25.8	123	2	JC2415	echicetin beta cha
14	168	24.2	40	2	S56006	tokaracetin alpha
15	168	24.2	166	1	RGHU1A	regenerating islet
16	168	24.2	166	2	A45751	pancreatic stone p
17	164.5	23.7	175	2	S29822	pancreatitis-assoc
18	158	22.7	173	2	B47148	reg II, regenerati
19	157.5	22.7	175	2	A41719	pancreatic stone p
20	155	22.3	165	2	A47148	reg I, regeneratin
21	154.5	22.2	175	2	A37194	pancreatic thread
22	153.5	22.1	175	2	A49616	pancreatitis-assoc
23	151	21.7	165	2	A28351	pancreatic stone p
24	147	21.2	166	1	RGHU1B	regenerating islet
25	144	20.7	40	2	S56007	tokaracetin beta c
26	143.5	20.6	912	2	A54423	brevican precursor
27	143	20.6	2124	2	A28452	proteoglycan core
28	143	20.6	2132	1	A55182	aggrecan precursor
29	142.5	20.5	883	2	S57653	brevican precursor
30	142.5	20.5	1463	2	A53210	phospholipase A2 r
31	142	20.4	2415	1	A39086	aggrecan precursor
32	141.5	20.4	330	2	T46256	brevican - human (
33	140.5	20.2	883	2	S49126	brevican precursor
34	140	20.1	135	2	A38609	lectin, galactose-
35	140	20.1	162	1	LNRC1	lectin BRA3-1 prec
36	140	20.1	174	2	S54979	pancreatitis-assoc
37	139	20.0	40	2	B56829	alboaggregin-B alp
38	139	20.0	162	1	LNRC3	lectin BRA3-2 prec
39	138	19.9	1340	2	A39808	proteoglycan core
40	138	19.9	1487	2	S48719	phospholipase-A(2)
41	138	19.9	2327	2	T42630	aggrecan - bovine
42	136.5	19.6	142	2	S78596	ovocleidin - chick
43	133.5	19.2	178	2	T29536	hypothetical prote
44	132.5	19.1	1450	2	T30273	hypothetical prote
45	132	19.0	2109	1	I50421	aggrecan precursor
46	131	18.8	1268	2	S52781	neurocan - mouse
47	130	18.7	147	2	A26697	echinoidin - sea u
48	130	18.7	1257	2	S28764	neurocan precursor
49	128.5	18.5	174	2	I83377	regenerating prote
50	127.5	18.3	1479	2	T42710	mannose receptor,
51	127	18.3	1643	2	T14274	versican precursor
52	127	18.3	2397	1	A55535	versican precursor
53	127	18.3	2409	1	A60979	versican precursor
54	127	18.3	3381	2	T42389	versican precursor
55	126	18.1	1326	2	B56395	secretory phosphol
56	126	18.1	1465	2	A56395	secretory phosphol
57	126	18.1	3562	2	A47171	chondroitin sulfat
58	125.5	18.1	172	2	S32489	lectin - Iberian r
59	122	17.6	280	2	T29200	hypothetical prote
60	121.5	17.5	1458	1	A49707	phospholipase A2 r
61	121	17.4	1455	1	A48925	mannose receptor p
62	121	17.4	1723	2	S58880	receptor DEC-205 -
63	120.5	17.3	174	1	A48689	pancreatitis-assoc
64	120.5	17.3	1456	1	A36563	mannose receptor p
65	118.5	17.1	616	2	T32131	hypothetical prote

ALIGNMENTS

RESULT 1
JC4329
coagulation factor IX-binding protein A chain - habu
C;Species: Trimeresurus flavoviridis (habu)
C;Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4329
R;Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
J. Biochem. 118, 965-973, 1995
A;Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flavo
A;Reference number: JC4329; MUID:96318509; PMID:8749314
A;Accession: JC4329
A;Molecule type: protein
A;Residues: 1-129 <ATO>
A;Cross-references: UNIPROT:Q7LZ71
C;Comment: This protein binds calcium.
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: anticoagulant; blood coagulation; calcium binding; venom
F;2-127/Domain: C-type lectin homology <LCH>
F;2-13,30-127,102-119/Disulfide bonds: #status predicted

Query Match 47.8%; Score 332.5; DB 2; Length 129;
Best Local Similarity 47.7%; Pred. No. 1.7e-27;
Matches 61; Conservative 23; Mismatches 35; Indels 9; Gaps 2;

```
Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|||||| : :|||||   ||  |||||:||||||||:|:|:| || ||  ::  | :
Db          1 DCPSGWSSYEGHCYKPFKLYKTWDDAERFCTEQAKGGHLVSIESAGEADFVAQLVTENIQ 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVDCE 113
                  |:||||||| | : |        ||:|||| ::      |  : ::|  |:|  : |
Db         61 NTKSYVWIGLRVQGKEKQCSSEWSDGSSVSYENWIEAESKTCLGLEKETGFRKWVNIYCG 120
```

```
Qy        114 QQHSFICK 121
              ||: |:|:
Db        121 QQNPFVCE 128
```

RESULT 2
A47267
botrocetin alpha chain - jararaca
N;Alternate names: two chain botrocetin alpha chain
C;Species: Bothrops jararaca (jararaca)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47267; B37958
R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator pu
A;Reference number: A47267; MUID:93157385; PMID:8430107
A;Accession: A47267
A;Molecule type: protein
A;Residues: 1-133 <USA>
A;Cross-references: UNIPROT:P22029
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:124085)
R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug
Biochemistry 30, 1957-1964, 1991
A;Title: Isolation and chemical characterization of two structurally and functionally di
A;Reference number: A37958; MUID:91129280; PMID:1993206
A;Accession: B37958
A;Molecule type: protein
A;Residues: 1-40 <FUJ>
C;Complex: heterodimer of alpha and beta (see PIR:B47267) chains
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemagglutinin; heterodimer; venom
F;2-128/Domain: C-type lectin homology <LCH>
F;2-13,30-128,103-120/Disulfide bonds: #status experimental
F;80/Disulfide bonds: interchain (to beta-75) #status experimental

  Query Match 44.7%; Score 311; DB 2; Length 133;
  Best Local Similarity 45.9%; Pred. No. 3e-25;
  Matches 61; Conservative 24; Mismatches 38; Indels 10; Gaps 3;

```
Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVET-ALEASFVDNVLYANK 61
              :|||||| :  ||| |:|:| || |||||||||||||:|::  : |  || :::  |
Db          1 DCPSGWSSYEGNCYKFFQQKMNWADAERFCSEQAKGGHLVSIKIYSKEKDFVGDLVTKNI 60

Qy         62 EYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVDC 112
              :    | ||||||:|| : |        ||:||||:|:    :|| : :|     |  : |
Db         61 QSSDLYAWIGLRVENKEKQCSSEWSDGSSVSYENVVERTVKKCFALEKDLGFVLWINLYC 120

Qy        113 EQQHSFICKFTRP 125
              |:: |:||   |
Db        121 AQKNPFVCKSPPP 133
```

RESULT 3
JC4690
coagulation factor IX/factor X-binding protein chain A precursor - habu
C;Species: Trimeresurus flavoviridis (habu)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: JC4690; A39332
R;Matsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.
Biochem. Biophys. Res. Commun. 220, 382-387, 1996
A;Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from s
A;Reference number: JC4690; MUID:96184662; PMID:8645314
A;Accession: JC4690
A;Molecule type: mRNA
A;Residues: 1-152 <MAT1>
A;Cross-references: UNIPROT:P23806; DDBJ:D83331; NID:g1402639; PIDN:BAA11887.1; PID:g140
A;Experimental source: venom
R;Atoda, H.; Hyuga, M.; Morita, T.
J. Biol. Chem. 266, 14903-14911, 1991
A;Title: The primary structure of coagulation factor IX/factor X-binding protein isolate
otein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.
A;Reference number: A39332; MUID:91332000; PMID:1831197
A;Accession: A39332
A;Status: preliminary
A;Molecule type: protein
A;Residues: 24-152 <ATO>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: anticoagulant; blood coagulation; glycoprotein; hemolymph; lectin
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-152/Product: factor IX/X binding protein chain A #status predicted <MAT>
F;25-150/Domain: C-type lectin homology <LCH>
F;25-36,53-150,125-142/Disulfide bonds: #status predicted

  Query Match 43.5%; Score 302.5; DB 2; Length 152;
  Best Local Similarity 44.5%; Pred. No. 2.7e-24;
  Matches 57; Conservative 25; Mismatches 37; Indels 9; Gaps 2;

```
Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :| ||||| : :||| |::  ||  ||| |:|||| ||:|:|:: || ||  ::  | :
Db         24 DCLSGWSSYEGHCYKAFEKYKTWEDAERVCTEQAKGAHLVSIESSGEADFVAQLVTQNMK 83

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVDCE 113
                |  |||||||| | : |        ||:|||| ::     |  : ::|  |:|  : |
Db         84 RLDFYIWIGLRVQGKVKQCNSEWSDGSSVSYENWIEAESKTCLGLEKETDFRKWVNIYCG 143

Qy        114 QQHSFICK 121
              ||: |:|:
Db        144 QQNPFVCE 151
```

RESULT 4
JC7134
agkisacutacin alpha chain precursor - sharp-nosed viper
N;Alternate names: fibrinogenlytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
C;Accession: JC7134; PC7037
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom
A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Accession: JC7134
A;Molecule type: mRNA
A;Residues: 1-152 <CHE>
A;Cross-references: UNIPROT:Q9DEF9; UNIPROT:Q9IAM1; UNIPROT:Q8JIW0; GB:AF176420
A;Experimental source: venom gland
A;Accession: PC7037
A;Molecule type: protein
A;Residues: 24-53;84-86;87-94;125-136;137-152 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-152/Product: agkisacutacin alpha chain #status experimental <MAT>

  Query Match 41.9%; Score 291.5; DB 2; Length 152;
  Best Local Similarity 43.8%; Pred. No. 3.8e-23;
  Matches 56; Conservative 23; Mismatches 40; Indels 9; Gaps 2;

```
Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :| ||||| : :||| |||  ||| || ||::|  ||||:|:|:: || || :::    :
Db         24 DCSSGWSSYEGHCYKVFKQSKTWADAESFCTKQVNGGHLVSIESSGEADFVAHLIAQKIK 83

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                 ::||||| ||| : |       |||||| :  :  :|  |  :|   :|    ||
Db         84 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISYENWIEEESKKCLGVHIETGFHKWENFYCE 143

Qy        114 QQHSFICK 121
              ||  |:|:
Db        144 QQDPFVCE 151
```

RESULT 5
PC7027
aggretin alpha chain - Malayan pit viper (fragment)
C;Species: Calloselasma rhodostoma (Malayan pit viper)

```
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: PC7027
R;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet a
A;Reference number: PC7027; MUID:99443731; PMID:10512747
A;Accession: PC7027
A;Molecule type: mRNA
A;Residues: 1-144 <CHU>
A;Cross-references: UNIPROT:Q9I841
A;Experimental source: venom gland
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; platelet aggregation; venom

  Query Match             41.4%;  Score 288;  DB 2;  Length 144;
  Best Local Similarity   43.8%;  Pred. No. 8.3e-23;
  Matches   57;  Conservative   21;  Mismatches   40;  Indels   12;  Gaps    4;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|  |||  |::||: | :: ||  ||:||  |  | || |:|:  || || : | : |:
Db         12 DCDFGWSPYDQHCYQAFNEQKTWDEAEKFCRAQENGAHLASIESNGEADFV-SWLISQKD 70

Qy         63 YLT--RYIWIGLRVQNKGQPC-------SSISYENLVD--PFECFMVSRDTRLREWFKVD 111
                |    |:||||| ||| | |       ||:|||||:|    :|  : : |  |:|
Db         71 ELADEDYVWIGLRAQNKEQQCSSEWSDGSSVSYENLIDLHTKKCGALEKLTGFRKWVNYY 130

Qy        112 CEQQHSFICK 121
              ||| |:|:||
Db        131 CEQMHAFVCK 140


RESULT 6
JC7135
agkisacutacin beta chain precursor - sharp-nosed viper
N;Alternate names: fibrinogenlytic venom protein
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
C;Accession: JC7135; PC7038
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom
A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Accession: JC7135
A;Molecule type: mRNA
A;Residues: 1-146 <CHE>
A;Cross-references: UNIPROT:Q8JIW1; GB:AF176421
A;Experimental source: venom gland
A;Accession: PC7038
A;Molecule type: protein
A;Residues: 24-50;59-83;102-107;112-114 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: agkisacutacin beta chain #status experimental <MAT>

  Query Match             35.8%;  Score 248.5;  DB 2;  Length 146;
  Best Local Similarity   42.4%;  Pred. No. 1.1e-18;
  Matches   53;  Conservative   20;  Mismatches   43;  Indels    9;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| : :||||| :  ||| ||:||::| || || |  :: || ||  |
Db         24 DCPSEWSSYEGHCYKPFDEPKTWADAEKFCTQQHKGSHLASFHSSEEADFV--VTLTTPS 81

Qy         63 YLTRYIWIGLR-VQN----KGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHS 117
                |  :||||: : |    |    : : |::  : ||| :||| |    ||  :||    |
Db         82 LKTDLVWIGLKNIWNGCYWKWSDGTKLDYKDWREQFEC-LVSR-TVNNEWLSMDCGTTCS 139

Qy        118 FICKF 122
              |:|||
Db        140 FVCKF 144


RESULT 7
JC5058
bitiscetin alpha chain - puff adder
N;Alternate names: von Willebrand factor modulator protein
C;Species: Bitis arietans (puff adder)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5058; JC5916
R;Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oze
submitted to JIPID, January 1997
A;Description: Complete amino acid sequence of bitiscetin, a novel von willebrand factor
A;Reference number: JC5058
A;Contents: snake venom
A;Accession: JC5058
A;Molecule type: protein
A;Residues: 1-131 <MAT>
A;Cross-references: UNIPROT:Q7LZK5
A;Experimental source: snake venom
R;Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oze
Res. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997
A;Title: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor modula
A;Reference number: JC5916
A;Accession: JC5916
A;Molecule type: protein
A;Residues: 1-131 <MA2>
A;Experimental source: venom
C;Comment: This protein is a modulator of a von Willebrand factor modulator.
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: venom
F;4-125/Domain: C-type lectin homology <LCH>

  Query Match             34.9%;  Score 242.5;  DB 2;  Length 131;
  Best Local Similarity   38.5%;  Pred. No. 4.3e-18;
  Matches   52;  Conservative   23;  Mismatches   45;  Indels   15;  Gaps    4;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  |    |||   :||| ||:  ||  ||:|| | :  ||| |:::  || ||  :
Db          1 DPGCLPDWSSYKGHCYKVFKKVGTWEDAEKFCVENS--GHLASIDSKEEADFVTKLA--- 55

Qy         61 KEYLTRYI---WIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKV 110
                : ||:::   |||||  ::| | |       ||: |||: :| :|| :   |  | |  :
Db         56 SQTLTKFVYDAWIGLRDESKTQQCSPQWTDGSSVVYENVDEPTKCFGLDVHTEYRTWTDL 115

Qy        111 DCEQQHSFICKFTRP 125
               | ::: ||||   |
Db        116 PCGEKNPFICKSRLP 130


RESULT 8
JC7105
aggretin beta chain - Malayan pit viper
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: JC7105
R;Chung, C.H.; Au, L.C.; Huang, T.P.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet ag
A;Reference number: PC7027; MUID:99443731; PMID:10512747
A;Accession: JC7105
A;Molecule type: mRNA
A;Residues: 1-146 <CHU>
A;Cross-references: UNIPROT:Q9I840
A;Experimental source: venom gland
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; platelet aggregation; venom

  Query Match             32.4%;  Score 225.5;  DB 2;  Length 146;
  Best Local Similarity   37.8%;  Pred. No. 2.9e-16;
  Matches   48;  Conservative   18;  Mismatches   48;  Indels   13;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|||||| : :||||| :   || |||||  | |  ||:| ::| || ||  |
Db         24 DCPSGWSSYEGHCYKPFNEPKNWADAERFCKLQPKHSHLVSFQSAEEADFV--VKLTRPR 81

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKVDCEQQ 115
```

```
                  :|:||   |    |       : ::|::  :  || :  |     ||  :||
Db         82 LKANLVWMGL--SNIWHGCNWQWSDGARLNYKDWQEQSEC-LAFRGVH-TEWLNMDCSST 137

Qy        116 HSFICKF 122
                ||:|||
Db        138 CSFVCKF 144


RESULT 9
B42972
coagulation factor X activating enzyme (EC 3.4.24.-) light chain - Russell's viper
C;Species: Vipera russelli (Russell's viper)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B42972
R;Takeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, S.
J. Biol. Chem. 267, 14109-14117, 1992
A;Title: Coagulation factor X activating enzyme from Russell's viper venom (RVV-X). A nc
A;Reference number: A42972; MUID:92332516; PMID:1629211
A;Contents: V. r. siamensis
A;Accession: B42972
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <TAK>
A;Cross-references: UNIPROT:Q7LZ72
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:108408)
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hydrolase; metalloproteinase; venom; zinc
F;4-121/Domain: C-type lectin homology <LCH>
F;4-15,32-121,98-113/Disulfide bonds: #status predicted

  Query Match             31.4%;  Score 218.5;  DB 2;  Length 123;
  Best Local Similarity   35.9%;  Pred. No. 1.3e-15;
  Matches   46;  Conservative   21;  Mismatches   48;  Indels   13;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              |:||||| | :::||| |     .|  ||:||:|| || ||:|: :  |  || |::  |
Db          2 LDCPSGWLSYEQHCYKGFNDLKNWTDAEKFCTEQKKGSHLVSLHSREEEEFVVNLISENL 61

Qy         62 EYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKVDCEQ 114
              ||     ||||   |  : |         :: |: | :   | ::   |  :||  : |
Db         62 EYPA--TWIGL--GNMWKDCRMEWSDRGNVKYKALAEESYCLIMI--THEKEWKSMTCNF 115

Qy        115 QHSFICKF 122
                :|||
Db        116 IAPVVCKF 123


RESULT 10
JC5059
bitiscetin beta chain - puff adder
C;Species: Bitis arietans (puff adder)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5059; JC5917
R;Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz
submitted to JIPID, January 1997
A;Description: Complete amino acid sequence of bitiscetin, a novel von willebrand factor
A;Reference number: JC5058
A;Accession: JC5059
A;Molecule type: protein
A;Residues: 1-125 <MAT>
A;Cross-references: UNIPROT:Q7LZK8
A;Experimental source: snake venom
R;Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz
Res. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997
A;Title: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor modul
A;Reference number: JC5916
A;Accession: JC5917
A;Molecule type: protein
A;Residues: 1-125 <MA2>
A;Experimental source: venom
C;Comment: This protein is a modulator of a von Willebrand factor modulator.
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: venom
F;4-121/Domain: C-type lectin homology <LCH>

  Query Match             28.3%;  Score 196.5;  DB 2;  Length 125;
  Best Local Similarity   34.1%;  Pred. No. 2.6e-13;
  Matches   44;  Conservative   22;  Mismatches   50;  Indels   13;  Gaps    4;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  |   |||   :||| || | ||| ||:|| |   ||||:|| :  |  |:  :  |
Db          1 DEGCLPDWSSYKGHCYKVFKVEKTWADAEKFCKELVNGGHLMSVNSREEGEFISKL--AL 58

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKVDCE 113
              ::      :||||   :  : |         : : |  | |   ||:   ::   :| :  |
Db         59 EKMRIVLVWIGL--SHFWRICPLRWTDGARLDYRALSDEPICFVA--ESFHNKWIQWTCN 114

Qy        114 QQHSFICKF 122
              :: ||:||:
Db        115 RKKSFVCKY 123


RESULT 11
JC4691
coagulation factor IX/factor X-binding protein chain A precursor - habu
C;Species: Trimeresurus flavoviridis (habu)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: JC4691; B39332; JC4330
R;Matsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.
Biochem. Biophys. Res. Commun. 220, 382-387, 1996
A;Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from sr
A;Reference number: JC4690; MUID:96184662; PMID:8645314
A;Accession: JC4691
A;Molecule type: mRNA
A;Residues: 1-146 <MAT1>
A;Cross-references: UNIPROT:P23807; DDBJ:D83332; NID:g1402641; PIDN:BAA11888.1; PID:g140
A;Experimental source: venom
R;Atoda, H.; Hyuga, M.; Morita, T.
J. Biol. Chem. 266, 14903-14911, 1991
A;Title: The primary structure of coagulation factor IX/factor X-binding protein isolatec
otein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.
A;Reference number: A39332; MUID:91332000; PMID:1831197
A;Accession: B39332
A;Molecule type: protein
A;Residues: 24-146 <ATO>
R;Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
J. Biochem. 118, 965-973, 1995
A;Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flavc
A;Reference number: JC4329; MUID:96318509; PMID:8749314
A;Accession: JC4330
A;Molecule type: protein
A;Residues: 24-146 <AT2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: anticoagulant; blood coagulation; lectin; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-146/Product: factor IX/X binding protein chain B #status predicted <MAT>
F;25-142/Domain: C-type lectin homology <LCH>
F;25-36,53-142,119-134/Disulfide bonds: #status predicted

  Query Match             27.7%;  Score 192.5;  DB 2;  Length 146;
  Best Local Similarity   33.1%;  Pred. No. 8.1e-13;
  Matches   42;  Conservative   22;  Mismatches   50;  Indels   13;  Gaps    4;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| : :||||| :   || || ||::|  ||||:| ::: || ||  |  | :
Db         24 DCPSDWSSYEGHCYKPFSEPKNWADAENFCTQQHAGGHLVSFQSSEEADFV--VKLAFQT 81

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKVDCEQQ 115
              :     |:||   |    |         : : |:   :  | : |   :    :|    |
Db         82 FGHSIFWMGL--SNVWNQCNWQWSNAAMLRYKAWAE--ESYCVYFKSTNNKWRSRACRMM 137

Qy        116 HSFICKF 122
                |:|:|
Db        138 AQFVCEF 144
```

RESULT 12
B47267
botrocetin beta chain - jararaca
N;Alternate names: two chain botrocetin beta chain
C;Species: Bothrops jararaca (jararaca)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B47267; C37958
R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator pu
A;Reference number: A47267; MUID:93157385; PMID:8430107
A;Accession: B47267
A;Molecule type: protein
A;Residues: 1-125 <USA>
A;Cross-references: UNIPROT:P22030
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:124086)
R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug
Biochemistry 30, 1957-1964, 1991
A;Title: Isolation and chemical characterization of two structurally and functionally di
A;Reference number: A37958; MUID:91129280; PMID:1993206
A;Accession: C37958
A;Molecule type: protein
A;Residues: 1-40 <FUJ>
C;Complex: heterodimer of alpha (see PIR:A47267) and beta chains
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemagglutinin; heterodimer; venom
F;2-121/Domain: C-type lectin homology <LCH>
F;2-13,30-121,98-113/Disulfide bonds: #status experimental
F;75/Disulfide bonds: interchain (to alpha-80) #status experimental

Query Match 27.6%; Score 191.5; DB 2; Length 125;
Best Local Similarity 35.1%; Pred. No. 8.6e-13;
Matches 46; Conservative 25; Mismatches 41; Indels 19; Gaps 8;

```
Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||  ||| : :||: ||: | |  || ||:||  | ||:| ::  || || ::     |
Db          1 DCPPDWSSYEGHCYRFFKEWMHWDDAEEFCTEQQTGAHLVSFQSKEEADFVRSL---TSE 57

Qy         63 YLT-RYIWIGLR-VQNKGQPC-------SSISYEN--LVDPFECFMVSRDTRLREWFKVD 111
                |    :|||  | ||   |           |::  |:  :|| : |: |   :|: :
Db         58 MLKGDVVWIGLSDVWNK---CRFEWTDGMEFDYDDYYLIAEYEC-VASKPTN-NKWWIIP 112

Qy        112 CEQQHSFICKF 122
               | :  :|:|:|
Db        113 CTRFKNFVCEF 123
```

RESULT 13
JC2415
echicetin beta chain - saw-scaled viper
C;Species: Echis carinatus (saw-scaled viper)
C;Date: 21-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JC2415
R;Peng, M.; Holt, J.C.; Niewiarowski, S.
Biochem. Biophys. Res. Commun. 205, 68-72, 1994
A;Title: Isolation, characterization and amino acid sequence of echicetin beta subunit,
A;Reference number: JC2415; MUID:95091801; PMID:7999097
A;Accession: JC2415
A;Molecule type: protein
A;Residues: 1-123 <PEN>
A;Cross-references: UNIPROT:P81996
A;Experimental source: venom
C;Comment: This protein inhibits agglutination of fixed platelets induced by several pla
llebrand factor and alboaggregins.
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: anticoagulant; dimer
F;2-119/Domain: C-type lectin homology <LCH>
F;2-13,30-119,96-111/Disulfide bonds: #status predicted

Query Match 25.8%; Score 179.5; DB 2; Length 123;
Best Local Similarity 30.4%; Pred. No. 1.5e-11;
Matches 38; Conservative 23; Mismatches 51; Indels 13; Gaps 4;

```
Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              |   ||  : |||| ||: | || ||:|| :| | |||:|   : |  |: :: :   :
Db          2 CLPDWSVYEGYCYKVFKERMNWADAEKFCMKQVKDGHLVSFRNSKEVDFMISLAFPMLK- 60

Qy         64 LTRYIWIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKVDCEQQH 116
                :||||   :  : |       : : |:   :   ||  :  |   :| :  |  :
Db         61 -MELVWIGL--SDYWRDCYWEWSDGAQLDYKAWDNERHCF--AAKTTDNQWMRRKCSGEF 115

Qy        117 SFICK 121
                |:||
Db        116 YFVCK 120
```

RESULT 14
S56006
tokaracetin alpha chain - Trimeresurus tokarensis (fragment)
N;Alternate names: platelet aggregation inhibitor; platelet antagonist
C;Species: Trimeresurus tokarensis
C;Date: 10-Oct-1995 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: S56006
R;Kawasaki, T.; Taniuchi, Y.; Hisamichi, N.; Fujimura, Y.; Suzuki, M.; Titani, K.; Sakai,
Biochem. J. 308, 947-953, 1995
A;Title: Tokaracetin, a new platelet antagonist that binds to platelet glycoprotein Ib ar
A;Reference number: S56006; MUID:97104297; PMID:8948455
A;Accession: S56006
A;Molecule type: protein
A;Residues: 1-40 <KAW>
A;Cross-references: UNIPROT:Q7LZK6
C;Superfamily: tetranectin; C-type lectin homology

Query Match 24.2%; Score 168; DB 2; Length 40;
Best Local Similarity 70.0%; Pred. No. 6.9e-11;
Matches 28; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

```
Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLL 42
              :|||||||  :||||||||  ||  ||||| || || ||:
Db          1 DCPSGWSSFKQYCYKPFKQLKTWEDAERFCLEQVKGAHLV 40
```

RESULT 15
RGHU1A
regenerating islet lectin 1-alpha precursor [validated] - human
N;Alternate names: lithostathine; pancreatic thread protein (PTP); reg I protein; reg1-al
N;Contains: pancreatic stone protein (PSP)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A35197; B28351; S12950; S02767; S02419; S00113; S01471; A25246
R;Watanabe, T.; Yonekura, H.; Terazono, K.; Yamamoto, H.; Okamoto, H.
J. Biol. Chem. 265, 7432-7439, 1990
A;Title: Complete nucleotide sequence of human reg gene and its expression in normal and
product of the gene.
A;Reference number: A35197; MUID:90237042; PMID:2332435
A;Accession: A35197
A;Molecule type: DNA
A;Residues: 1-166 <WAT>
A;Cross-references: UNIPROT:P05451; GB:J05412
R;Terazono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamotc
J. Biol. Chem. 263, 2111-2114, 1988
A;Title: A novel gene activated in regenerating islets.
A;Reference number: A92704; MUID:88115343; PMID:2963000
A;Accession: B28351
A;Molecule type: mRNA
A;Residues: 1-166 <TER>
A;Cross-references: GB:M18963; NID:g190978; PIDN:AAA36558.1; PID:g190979
R;Itoh, T.; Tsuzuki, H.; Katoh, T.; Teraoka, H.; Matsumoto, K.; Yoshida, N.; Terazono, K.
FEBS Lett. 272, 85-88, 1990
A;Title: Isolation and characterization of human reg protein produced in Saccharomyces ce
A;Reference number: S12950; MUID:91032149; PMID:2226837
A;Accession: S12950
A;Molecule type: protein
A;Residues: 23-52;160-166 <ITO>

A;Note: sequence determined from protein isolated after human cDNA sequence was cloned a
R;de Caro, A.M.; Adrich, Z.; Fournet, B.; Capon, C.; Bonicel, J.J.; de Caro, J.D.; Rover
Biochim. Biophys. Acta 994, 281-284, 1989
A;Title: N-terminal sequence extension in the glycosylated forms of human pancreatic stc
A;Reference number: S02767; MUID:89150292; PMID:2493268
A;Accession: S02767
A;Molecule type: protein
A;Residues: 23-47 <DEC>
R;Rouimi, P.; de Caro, J.; Bonicel, J.; Rovery, M.; de Caro, A.
FEBS Lett. 229, 171-174, 1988
A;Title: The disulfide bridges of the immunoreactive forms of human pancreatic stone prc
A;Reference number: S02419; MUID:88152214; PMID:3345835
A;Accession: S02419
A;Molecule type: protein
A;Residues: 63-72;125-139;150-157;160-166 <ROU>
A;Note: disulfide bonds
R;de Caro, A.M.; Bonicel, J.J.; Rouimi, P.; de Caro, J.D.; Sarles, H.; Rovery, M.
Eur. J. Biochem. 168, 201-207, 1987
A;Title: Complete amino acid sequence of an immunoreactive form of human pancreatic ston
A;Reference number: S00113; MUID:88029417; PMID:3665916
A;Accession: S00113
A;Molecule type: protein
A;Residues: 34-166 <DE1>
R;Rouimi, P.; Bonicel, J.; Rovery, M.; de Caro, A.
FEBS Lett. 216, 195-199, 1987
A;Title: Cleavage of the Arg-Ile bond in the native polypeptide chain of human pancreati
A;Reference number: S01471; MUID:87219142; PMID:3108036
A;Accession: S01471
A;Molecule type: protein
A;Residues: 33-48 <RO2>
R;Montalto, G.; Bonicel, J.; Multigner, L.; Rovery, M.; Sarles, H.; De Caro, A.
Biochem. J. 238, 227-232, 1986
A;Title: Partial amino acid sequence of human pancreatic stone protein, a novel pancreat
A;Reference number: A25246; MUID:87099950; PMID:3541906
A;Accession: A25246
A;Molecule type: protein
A;Residues: 34-73,'X',75-87,'R',89-98 <MON>
C;Comment: This protein is found in pancreatic calculi of mammals. The tryptic-like clea
C;Comment: Intact regenerating islet lectin 1-alpha, lithostathine, inhibits the growth
C;Genetics:
A;Gene: GDB:REG1A; REG
A;Cross-references: GDB:132455; OMIM:167770
A;Map position: 2p12-2p12
A;Introns: 22/1; 61/3; 107/3; 145/1
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: glycoprotein; lectin; pancreas; pyroglutamic acid
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-166/Product: regenerating islet lectin 1-alpha #status experimental <MAT>
F;34-166/Product: pancreatic stone protein #status experimental <MAT2>
F;36-162/Domain: C-type lectin homology <LCH>
F;23/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F;27/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;33-34/Cleavage site: Arg-Ile (trypsin) #status experimental
F;36-47,64-162,137-154/Disulfide bonds: #status experimental

Query Match 24.2%; Score 168; DB 1; Length 166;
Best Local Similarity 31.1%; Pred. No. 3.4e-10;
Matches 42; Conservative 25; Mismatches 50; Indels 18; Gaps 5;

Qy 2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
Db 34 ISCPEGTNAYRSYCYYFNEDRETWVDADLYC-QNMNSGNLVSVLTQAEGAFVASLI---K 89

Qy 62 EYLTR--YIWIGLRVQNKGQ-----PCSSISYE-------NLVDPFECFMVSRDTRLREW 107
Db 90 ESGTDDFNVWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKW 149

Qy 108 FKVDCEQQHSFICKF 122
Db 150 KDVPCEDKFSFVCKF 164

RESULT 16
A45751
pancreatic stone protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
C;Accession: A45751
R;Giorgi, D.; Bernard, J.P.; Rouquier, S.; Iovanna, J.; Sarles, H.; Dagorn, J.C.
J. Clin. Invest. 84, 100-106, 1989
A;Title: Secretory pancreatic stone protein messenger RNA. Nucleotide sequence and expres
A;Reference number: A45751; MUID:89292148; PMID:2525567
A;Accession: A45751
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-166 <GIO>
A;Cross-references: UNIPROT:P05451; GB:M27190; NID:g623412; PIDN:AAA60546.1; PID:g623413
C;Superfamily: tetranectin; C-type lectin homology
F;36-162/Domain: C-type lectin homology <LCH>

Query Match 24.2%; Score 168; DB 2; Length 166;
Best Local Similarity 31.1%; Pred. No. 3.4e-10;
Matches 42; Conservative 25; Mismatches 50; Indels 18; Gaps 5;

Qy 2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
Db 34 ISCPEGTNAYRSYCYYFNEDRETWVDADLYC-QNMNSGNLVSVLTQAEGAFVASLI---K 89

Qy 62 EYLTR--YIWIGLRVQNKGQ-----PCSSISYE-------NLVDPFECFMVSRDTRLREW 107
Db 90 ESGTDDFNVWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKW 149

Qy 108 FKVDCEQQHSFICKF 122
Db 150 KDVPCEDKFSFVCKF 164

RESULT 17
S29822
pancreatitis-associated protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S29822
R;Itoh, T.; Teraoka, H.
Biochim. Biophys. Acta 1172, 184-186, 1993
A;Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homologu
A;Reference number: S29821; MUID:93176807; PMID:7679928
A;Accession: S29822
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-175 <ITO>
A;Cross-references: UNIPROT:P35230; GB:D13509; NID:g286106; PIDN:BAA02727.1; PID:g286107
C;Superfamily: tetranectin; C-type lectin homology
F;40-171/Domain: C-type lectin homology <LCH>

Query Match 23.7%; Score 164.5; DB 2; Length 175;
Best Local Similarity 30.0%; Pred. No. 8.3e-10;
Matches 42; Conservative 20; Mismatches 57; Indels 21; Gaps 4;

Qy 2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDN-VLYAN 60
Db 38 ISCPKGSQAYGSYCYALFQIPQTWFDAELAC-QKRPGGHLVSVLNSAEASFLSSMVKRTG 96

Qy 61 KEYLTRYIWIGLRVQNKGQPCSSISYE-----------------NLVDPFECFMVSRDTR 103
Db 97 NSY--QYTWIGLHDPTLGAEPNGGGWEWSNNDVMNYFNWERNPSTALDRAFCGSLSRASG 154

Qy 104 LREWFKVDCEQQHSFICKFT 123
Db 155 FLKWRDMTCEVKLPYVCKFT 174

RESULT 18
B47148
reg II, regenerating islet cells - mouse
C;Species: Mus musculus (house mouse)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: B47148
R;Unno, M.; Yonekura, H.; Nakagawara, K.; Watanabe, T.; Miyashita, H.; Moriizumi, S.; Ok
J. Biol. Chem. 268, 15974-15982, 1993
A;Title: Structure, chromosomal localization, and expression of mouse reg genes, reg I a
A;Reference number: A47148; MUID:93340209; PMID:8340418
A;Accession: B47148
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <UNN>
A;Cross-references: UNIPROT:Q08731; GB:D14011; NID:g391773; PIDN:BAA03112.1; PID:g391774
C;Genetics:
A;Introns: 22/1; 68/3; 114/3; 152/1
C;Superfamily: tetranectin; C-type lectin homology
F;43-169/Domain: C-type lectin homology <LCH>
F;43-54,71-169,144-161/Disulfide bonds: #status predicted

Query Match 22.7%; Score 158; DB 2; Length 173;
Best Local Similarity 28.9%; Pred. No. 3.9e-09;
Matches 39; Conservative 27; Mismatches 51; Indels 18; Gaps 5;

```
Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : ||  | ::   |||   :  :||  |: || :    |||:|: :  |::|| :::   |
Db         41 INCPEGANAYGSYCYYLIEDRLTWGEADLFC-QNMNAGHLVSILSQAESNFVASLV---K 96

Qy         62 EYLT--RYIWIGLR--VQNKGQPCSSISY----------ENLVDPFECFMVSRDTRLREW 107
              |  |    :| ||     |:    || |           :  :   |  :: :|  ::|
Db         97 ESGTTASNVWTGLHDPKSNRRWHWSSGSLFLFKSWATGAPSTANRGYCVSLTSNTAYKKW 156

Qy        108 FKVDCEQQHSFICKF 122
                :|| |:||:|||
Db        157 KDENCEAQYSFVCKF 171
```

RESULT 19
A41719
pancreatic stone protein 2 precursor - rat
N;Alternate names: pancreatitis-associated protein; regenerating protein 2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 09-Jul-2004
C;Accession: A37456; A59313; I51899; JC1257; A41719
R;Dusetti, N.J.; Frigerio, J.M.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.
J. Biol. Chem. 268, 14470-14475, 1993
A;Title: Structural organization of the gene encoding the rat pancreatitis-associated pr
on domain-containing genes.
A;Reference number: A37456; MUID:93300847; PMID:8314803
A;Accession: A37456
A;Molecule type: DNA
A;Residues: 1-175 <DUS1>
A;Cross-references: UNIPROT:P25031; GB:L07127; NID:g349550
A;Experimental source: strain Wistar; tissue type liver
A;Note: only intron/exon boundaries are shown; exon I and the beginning of exon II are d
ension of the open reading frame to an ATG codon in exon I is shown in accession A59313
R;Dusetti, N.J.; Frigerio, J.M.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.
submitted to GenBank, August 1993
A;Reference number: A59313
A;Accession: A59313
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 'MMRVK',1-175 <DUS2>
A;Cross-references: GB:L07127; NID:g349550; PIDN:AAA41805.1; PID:g349551
A;Note: an incorrect initiation codon was used
R;Iovanna, J.L.; Keim, V.; Bosshard, A.; Orelle, B.; Frigerio, J.M.; Dusetti, N.; Dagorn
Am. J. Physiol. 265, G611-G618, 1993
A;Title: PAP, a pancreatic secretory protein induced during acute pancreatitis, is expre
A;Reference number: I51899; MUID:94056762; PMID:8238345
A;Accession: I51899
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-175 <IOV1>
A;Cross-references: GB:M98049; NID:g393210; PIDN:AAA16341.1; PID:g393211
A;Note: in Genbank entry RATPAPC, release 113.0, the source is designated as Rattus ratt
R;Kamimura, T.; West, C.; Beutler, E.
Gene 118, 299-300, 1992
A;Title: Sequence of a cDNA clone encoding a rat Reg-2 protein.
A;Reference number: JC1257; MUID:92380521; PMID:1511905
A;Accession: JC1257
A;Molecule type: mRNA
A;Residues: 1-6,'S',8-175 <KAM>
A;Cross-references: GB:S43715; NID:g254694; PIDN:AAB23103.1; PID:g254695
R;Iovanna, J.; Orelle, B.; Keim, V.; Dagorn, J.C.
J. Biol. Chem. 266, 24664-24669, 1991
A;Title: Messenger RNA sequence and expression of rat pancreatitis-associated protein, a
A;Reference number: A41719; MUID:92105133; PMID:1722211
A;Accession: A41719
A;Molecule type: mRNA
A;Residues: 1-175 <IOV2>
A;Cross-references: GB:M55149; NID:g206030; PIDN:AAA41807.1; PID:g206031
A;Note: the amino-terminal residue of the mature protein was identified as Glu
C;Genetics:
A;Gene: pap
A;Introns: 26/1; 65/3; 111/3; 154/1
A;Note: the first intron occurs before the initiator codon
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: lectin; pancreas
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-175/Product: pancreatitis-associated protein #status experimental <MAT>
F;40-171/Domain: C-type lectin homology <LCH>
F;40-51,68-171,146-163/Disulfide bonds: #status predicted

Query Match 22.7%; Score 157.5; DB 2; Length 175;
Best Local Similarity 30.2%; Pred. No. 4.5e-09;
Matches 42; Conservative 21; Mismatches 57; Indels 19; Gaps 5;

```
Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || |  :   |||  |:   ||  ||  | :: : |||:||    ||||: :::  |
Db         38 ISCPKGSQAYGSYCYALFQIPQTWFDAELACQKRPE-GHLVSVLNVAEASFLASMV-KNT 95

Qy         62 EYLTRYIWIGLRVQN-KGQPCSS---------ISYEN-------LVDPFECFMVSRDTRL 104
                :| ||||      |:|              ::| |       :|   |  :|| :
Db         96 GNSYQYTWIGLHDPTLGGEPNGGGWEWSNNDIMNYVNWERNPSTALDRGFCGSLSRSSGF 155

Qy        105 REWFKVDCEQQHSFICKFT 123
                |    || :  ::||||
Db        156 LRWRDTTCEVKLPYVCKFT 174
```

RESULT 20
A47148
reg I, regenerating islet cells - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A47148
R;Unno, M.; Yonekura, H.; Nakagawara, K.; Watanabe, T.; Miyashita, H.; Moriizumi, S.; Oka
J. Biol. Chem. 268, 15974-15982, 1993
A;Title: Structure, chromosomal localization, and expression of mouse reg genes, reg I ar
A;Reference number: A47148; MUID:93340209; PMID:8340418
A;Accession: A47148
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-165 <UNN>
A;Cross-references: UNIPROT:P43137; GB:D14010; NID:g391771; PIDN:BAA03111.1; PID:g391772
C;Genetics:
A;Introns: 21/1; 60/3; 106/3; 144/1
C;Superfamily: tetranectin; C-type lectin homology
F;35-161/Domain: C-type lectin homology <LCH>
F;35-46,63-161,136-153/Disulfide bonds: #status predicted

Query Match 22.3%; Score 155; DB 2; Length 165;
Best Local Similarity 27.5%; Pred. No. 7.7e-09;
Matches 39; Conservative 26; Mismatches 45; Indels 32; Gaps 5;

```
Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || |  ::   |||   :  :||| |: || :    |:|:|| :  | :|| :::   |
Db         33 ISCPEGSNAYSSYCYYFTEDRLTWADADLFC-QNMNSGYLVSVLSQAEGNFVASLI---K 88
```

```
Qy         62 EYLT--RYIWIGLRVQNK------------------GQPCSSISYENLVDPFECFMVSR 100
              |  |    :| ||    :                  | | ||      :   |  ::
Db         89 ESGTTDANVWTGLHDPKRNRRWHWSSGSLFLYKSWATGSPNSS-------NRGYCVSLTS 141

Qy        101 DTRLREWFKVDCEQQHSFICKF 122
              :|  ::|   :|: |:||:|||
Db        142 NTGYKKWKDDNCDAQYSFVCKF 163


RESULT 21
A37194
pancreatic thread protein precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 09-Jul-2004
C;Accession: A37194; A53897
R;de la Monte, S.M.; Ozturk, M.; Wands, J.R.
J. Clin. Invest. 86, 1004-1013, 1990
A;Title: Enhanced expression of an exocrine pancreatic protein in Alzheimer's disease an
A;Reference number: A37194; MUID:90368981; PMID:2394826
A;Accession: A37194
A;Molecule type: mRNA
A;Residues: 1-175 <DEL>
A;Cross-references: UNIPROT:P23132; GB:M59794; NID:g163648; PIDN:AAA30750.1; PID:g163649
R;Cai, L.; Harris, W.R.; Marshak, D.R.; Gross, J.; Crabb, J.W.
J. Protein Chem. 9, 623-632, 1990
A;Title: Structural analysis of bovine pancreatic thread protein.
A;Reference number: A53897; MUID:91197388; PMID:2085387
A;Accession: A53897
A;Molecule type: protein
A;Residues: 38-138;141-175 <CAI>
C;Comment: The purified protein undergoes a reversible globule-fibril transformation and
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; extracellular protein; pancreas
F;38-138/Product: pancreatic thread protein chain A #status experimental <ACH>
F;40-171/Domain: C-type lectin homology <LCH>
F;141-175/Product: pancreatic thread protein chain B #status experimental <BCH>

  Query Match             22.2%;  Score 154.5;  DB 2;  Length 175;
  Best Local Similarity   30.2%;  Pred. No. 9.2e-09;
  Matches   42;  Conservative   19;  Mismatches   59;  Indels   19;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : ||||  :   :||  ||   ||  |:  | ::   |||:|| :  | ||| : |  |
Db         38 ISCPSGSMAYRSHCYALFKTPKTWMDADIAC-QKRPSGHLVSVLSGAEESFVAS-LVRNN 95

Qy         62 EYLTRYIWIGLRVQNKGQPCSSISYE-------NLV----------DPFECFMVSRDTRL 104
                |||||    :|   ::  :|       | |           |  |  :|| :
Db         96 LNTQSDIWIGLHDPTEGSEANAGGWEWISNDVLNYVAWETDPAAISSPGYCGSLSRSSGY 155

Qy        105 REWFKVDCEQQHSFICKFT 123
              :|   :|     ::||||
Db        156 LKWRDHNCNLNLPYVCKFT 174


RESULT 22
A49616
pancreatitis-associated protein precursor - human
N;Alternate names: C-type lectin; pancreatic stone protein homolog HIP
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: A49616; A44931; S29821; S48197; I55580
R;Dusetti, N.J.; Frigerio, J.M.; Fox, M.F.; Swallow, D.M.; Dagorn, J.C.; Iovanna, J.L.
Genomics 19, 108-114, 1994
A;Title: Molecular cloning, genomic organization, and chromosomal localization of the hu
A;Reference number: A49616; MUID:94245143; PMID:8188210
A;Accession: A49616
A;Molecule type: DNA
A;Residues: 1-175 <DUS>
A;Cross-references: UNIPROT:Q06141; GB:L15533; NID:g482908; PIDN:AAA60020.1; PID:g482909
R;Lasserre, C.; Christa, L.; Simon, M.T.; Vernier, P.; Brechot, C.
Cancer Res. 52, 5089-5095, 1992
A;Title: A novel gene (HIP) activated in human primary liver cancer.
A;Reference number: A44931; MUID:92386513; PMID:1325291
A;Accession: A44931
A;Molecule type: mRNA
A;Residues: 1-175 <LAS>
A;Cross-references: GB:X68641; NID:g312806; PIDN:CAA48605.1; PID:g312807
A;Experimental source: hepatocellular carcinoma
A;Note: sequence extracted from NCBI backbone (NCBIN:113007, NCBIP:113008)
R;Itoh, T.; Teraoka, H.
Biochim. Biophys. Acta 1172, 184-186, 1993
A;Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homologu
A;Reference number: S29821; MUID:93176807; PMID:7679928
A;Accession: S29821
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-175 <ITO>
A;Cross-references: GB:D13510; NID:g285970; PIDN:BAA02728.1; PID:g285971
R;Lasserre, C.; Simon, M.T.; Ishikawa, H.; Diriong, S.; Nguyen, V.C.; Christa, L.; Vernie
Eur. J. Biochem. 224, 29-38, 1994
A;Title: Structural organization and chromosomal localization of a human gene (HIP/PAP) e
A;Reference number: S48197; MUID:94357229; PMID:8076648
A;Accession: S48197
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-175 <LA2>
R;Orelle, B.; Keim, V.; Masciotra, L.; Dagorn, J.C.; Iovanna, J.L.
J. Clin. Invest. 90, 2284-2291, 1992
A;Title: Human pancreatitis-associated protein. Messenger RNA cloning and expression in p
A;Reference number: I55580; MUID:93107309; PMID:1469087
A;Accession: I55580
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-175 <RES>
A;Cross-references: GB:S51768; NID:g262368; PIDN:AAB24642.1; PID:g262369
C;Genetics:
A;Gene: GDB:PAP; HIP
A;Cross-references: GDB:136839; OMIM:167805
A;Map position: 2p12-2p12
A;Introns: 26/1; 65/3; 111/3; 154/1
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: acute phase; extracellular protein; pancreas
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-175/Product: pancreatitis-associated protein #status predicted <MAT>
F;40-171/Domain: C-type lectin homology <LCH>
F;40-51,68-171,146-163/Disulfide bonds: #status predicted

  Query Match             22.1%;  Score 153.5;  DB 2;  Length 175;
  Best Local Similarity   25.7%;  Pred. No. 1.2e-08;
  Matches   36;  Conservative   24;  Mismatches   59;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :   :||  |   :|  |:  | ::   |:|:|| :  | ||| ::: :
Db         38 IRCPKGSKAYGSHCYALFLSPKSWTDADLAC-QKRPSGNLVSVLSGAEGSFVSSLVKSIG 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                |   |:||||    :|   :   :|                :  |  |  :|| |
Db         97 NSY--SYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYFAWERNPSTISSPGHCASLSRSTA 154

Qy        104 LREWFKVDCEQQHSFICKFT 123
                 |   :|  :  ::||||
Db        155 FLRWKDYNCNVRLPYVCKFT 174


RESULT 23
A28351
pancreatic stone protein precursor - rat
N;Alternate names: lithostathine
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A28351; A39081; PL0147; S34618
R;Terazono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamotc
J. Biol. Chem. 263, 2111-2114, 1988
A;Title: A novel gene activated in regenerating islets.
A;Reference number: A92704; MUID:88115343; PMID:2963000
A;Accession: A28351
```

A;Molecule type: mRNA
A;Residues: 1-165 <TER>
A;Cross-references: UNIPROT:P10758; GB:M18962; NID:g206604; PIDN:AAA42028.1; PID:g206605
R;Rouquier, S.; Verdier, J.M.; Iovanna, J.; Dagorn, J.C.; Giorgi, D.
J. Biol. Chem. 266, 786-791, 1991
A;Title: Rat pancreatic stone protein messenger RNA. Abundant expression in mature exocr
A;Reference number: A39081; MUID:91093273; PMID:1985964
A;Accession: A39081
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-165 <ROU>
A;Cross-references: GB:M62930; GB:J05722; NID:g206462; PIDN:AAA41974.1; PID:g206463
R;Adrich, Z.; De Caro, A.M.; Guidoni, A.A.; Woudstra, M.E.; Rovery, M.
Comp. Biochem. Physiol. B 93, 793-797, 1989
A;Title: Characterization in rat pancreatic juice of a protein homologous to the human p
A;Reference number: PL0147; MUID:90031455; PMID:2680252
A;Accession: PL0147
A;Molecule type: protein
A;Residues: 22-69 <ADR>
A;Experimental source: pancreas
R;Dusetti, N.J.; Frigerio, J.M.; Dagorn, J.C.; Iovanna, J.L.
Biochim. Biophys. Acta 1174, 99-102, 1993
A;Title: Rapid PCR cloning and sequence determination of the rat lithostathine gene.
A;Reference number: S34618; MUID:93326645; PMID:7916640
A;Accession: S34618
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-165 <DUS>
A;Cross-references: EMBL:L07512; NID:g393208; PIDN:AAA41533.1; PID:g393209
C;Comment: This protein is found in pancreatic calculi of mammals. A peptide bond betwee
rotein into an insoluble protein at a neutral pH of 5.5 to 7.5.
C;Genetics:
A;Introns: 21/1; 60/3; 106/3; 144/1
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: pyroglutamic acid
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-165/Product: pancreatic stone protein #status predicted <MAT>
F;35-161/Domain: C-type lectin homology <LCH>
F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen

  Query Match 21.7%; Score 151; DB 2; Length 165;
  Best Local Similarity 29.6%; Pred. No. 2e-08;
  Matches 40; Conservative 26; Mismatches 51; Indels 18; Gaps 5;

```
Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || | ::   |||   :  ::|| |: || :    |:|:|| :  | :|: :::   |
Db         33 ITCPEGSNAYSSYCYYFMEDHLSWAEADLFC-QNMNSGYLVSVLSQAEGNFLASLI---K 88

Qy         62 EYLT--RYIWIGLR--VQNKGQPCSSIS----------YENLVDPFECFMVSRDTRLREW 107
              |  |    :||||     |:    || |          | |  :   |  |: ::  ::|
Db         89 ESGTTAANVWIGLHDPKNNRRWHWSSGSLFLYKSWDTGYPNNSNRGYCVSVTSNSGYKKW 148

Qy        108 FKVDCEQQHSFICKF 122
                |: | ||:|||
Db        149 RDNSCDAQLSFVCKF 163
```

RESULT 24
RGHU1B
regenerating islet lectin 1-beta precursor - human
N;Alternate names: reg-related protein; reg1-beta protein
N;Contains: pancreatic stone protein (PSP)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S34591; S42729; A44712
R;Bartoli, C.; Gharib, B.; Giorgi, D.; Sansonetti, A.; Dagorn, J.C.; Berge-Lefranc, J.L.
FEBS Lett. 327, 289-293, 1993
A;Title: A gene homologous to the reg gene is expressed in the human pancreas.
A;Reference number: S34591; MUID:93351647; PMID:8348956
A;Accession: S34591
A;Molecule type: DNA
A;Residues: 1-166 <BAR>
A;Cross-references: UNIPROT:P48304; GB:L08010; NID:g307368; PIDN:AAA18204.1; PID:g487726
A;Note: this gene appears to be expressed in pancreas and liver
R;Moriizumi, S.; Watanabe, T.; Unno, M.; Nakagawara, K.; Suzuki, Y.; Miyashita, H.; Yonek
Biochim. Biophys. Acta 1217, 199-202, 1994
A;Title: Isolation, structural determination and expression of a novel reg gene, human re
A;Reference number: S42729; MUID:94153997; PMID:8110835
A;Accession: S42729
A;Molecule type: mRNA
A;Residues: 1-166 <MOR>
A;Cross-references: GB:D16816; NID:g474305; PIDN:BAA04091.1; PID:g474306
A;Accession: A44712
A;Molecule type: DNA
A;Residues: 1-166 <MO2>
A;Cross-references: GB:D17291; NID:g474307; PIDN:BAA04124.1; PID:g474308
C;Comment: This protein is found in pancreatic calculi of mammals. The tryptic-like cleav
C;Genetics:
A;Gene: GDB:REG1B; REG1
A;Cross-references: GDB:342079
A;Map position: 2p12-2p12
A;Introns: 22/1; 61/3; 107/3; 145/1
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: glycoprotein; lectin; pancreas; pyroglutamic acid
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-166/Product: regenerating islet lectin 1beta #status predicted <MAT>
F;34-166/Product: pancreatic stone protein #status predicted <MAT2>
F;36-162/Domain: C-type lectin homology <LCH>
F;23/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;27/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;33-34/Cleavage site: Arg-Ile (trypsin) #status predicted
F;36-47,64-162,137-154/Disulfide bonds: #status predicted

  Query Match 21.2%; Score 147; DB 1; Length 166;
  Best Local Similarity 28.1%; Pred. No. 5.3e-08;
  Matches 38; Conservative 27; Mismatches 52; Indels 18; Gaps 5;

```
Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || | ::   |||   :  ||  |: :| :    |:|:|| |  | :|| :::   |
Db         34 ISCPEGTNAYRSYCYYFNEDPETWVDADLYC-QNMNSGNLVSVLTQAEGAFVASLI---K 89

Qy         62 EYLT--RYIWIGLRVQNKGQ-----PCSSISYE-------NLVDPFECFMVSRDTRLREW 107
              |  |    :||||    | :       | :||:       :  :   |  ::  :  ::|
Db         90 ESSTDDSNVWIGLHDPKKNRRWHWSSGSLVSYKSWDTGSPSSANAGYCASLTSCSGFKKW 149

Qy        108 FKVDCEQQHSFICKF 122
                ||:: ||:|||
Db        150 KDESCEKKFSFVCKF 164
```

RESULT 25
S56007
tokaracetin beta chain - Trimeresurus tokarensis (fragment)
N;Alternate names: platelet aggregation inhibitor; platelet antagonist
C;Species: Trimeresurus tokarensis
C;Date: 10-Oct-1995 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: S56007
R;Kawasaki, T.; Taniuchi, Y.; Hisamichi, N.; Fujimura, Y.; Suzuki, M.; Titani, K.; Sakai,
Biochem. J. 308, 947-953, 1995
A;Title: Tokaracetin, a new platelet antagonist that binds to platelet glycoprotein Ib ar
A;Reference number: S56006; MUID:97104297; PMID:8948455
A;Accession: S56007
A;Molecule type: protein
A;Residues: 1-40 <KAW>
A;Cross-references: UNIPROT:Q7LZI6

  Query Match 20.7%; Score 144; DB 2; Length 40;
  Best Local Similarity 56.4%; Pred. No. 2.2e-08;
  Matches 22; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

```
Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHL 41
              :||| ||| | :||: |:|:| |  ||:||::| || ||
Db          1 DCPSDWSSYDEHCYRVFQQKMNWEDAEKFCTQQHKGXHL 39
```

RESULT 26

```
A54423
brevican precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A54423; S41914
R;Yamada, H.; Watanabe, K.; Shimonaka, M.; Yamaguchi, Y.
J. Biol. Chem. 269, 10119-10126, 1994
A;Title: Molecular cloning of brevican, a novel brain proteoglycan of the aggrecan/versi
A;Reference number: A54423; MUID:94193597; PMID:8144512
A;Accession: A54423
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-912 <YAM>
A;Cross-references: UNIPROT:Q28062; GB:X75887; NID:g452820; PIDN:CAA53481.1; PID:g452821
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
F;50-139/Domain: immunoglobulin homology <IMM>
F;174-251/Domain: link protein repeat homology <LNK1>
F;272-353/Domain: link protein repeat homology <LNK2>
F;651-682/Domain: EGF homology <EGF>
F;689-809/Domain: C-type lectin homology <LCH>
F;816-872/Domain: complement factor H repeat homology <FHD>

  Query Match             20.6%;  Score 143.5;  DB 2;  Length 912;
  Best Local Similarity   28.8%;  Pred. No. 8.2e-07;
  Matches   46;  Conservative   10;  Mismatches   51;  Indels   53;  Gaps    7;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              |  || :    ||| |    :|  ||  |  :  | ||| |: |  |  |::|
Db        689 CSPGWDAFQGACYKHFSARRSWEEAENKC--RMYGAHLASISTPEEQDFINN-------R 739

Qy         64 LTRYIWIGLRVQ------------------NKGQPCS-SISYENLVDPFECFMVSRDTR 103
                | ||||  :                  | ||| |  :| || |     ||  |
Db        740 YREYQWIGLNDRTIEGDFLWSDGVPLLYENWNPGQPDSYFLSGENCV-----VMVWHDQ- 793

Qy        104 LREWFKVDCEQQHSFICK----------------FTRPR 126
                :|  | |    |: ||                | |||
Db        794 -GQWSDVPCNYHLSYTCKMGLVSCGPPPELPLAEVFGRPR 832


RESULT 27
A28452
proteoglycan core protein precursor, cartilage - rat
N;Alternate names: aggrecan
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A92623; A23835; A28453; A28095; A28452
R;Doege, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J. Biol. Chem. 262, 17757-17767, 1987
A;Title: Complete primary structure of the rat cartilage proteoglycan core protein deduc
A;Reference number: A92623; MUID:88087070; PMID:3693370
A;Accession: A92623
A;Molecule type: mRNA
A;Residues: 1-2124 <DOE>
A;Cross-references: UNIPROT:P07897
R;Doege, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y.
J. Biol. Chem. 263, 10040a, 1988
A;Reference number: A30069
A;Contents: annotation; revision to residue 698
R;Doege, K.; Fernandez, P.; Hassell, J.R.; Sasaki, M.; Yamada, Y.
J. Biol. Chem. 261, 8108-8111, 1986
A;Title: Partial cDNA sequence encoding a globular domain at the C terminus of the rat c
A;Reference number: A23835; MUID:86250698; PMID:2424893
A;Accession: A23835
A;Molecule type: mRNA
A;Residues: 1856-2124 <DO2>
A;Cross-references: GB:M13518; NID:g206104; PIDN:AAA41836.1; PID:g206105
R;Neame, P.J.; Christner, J.E.; Baker, J.R.
J. Biol. Chem. 262, 17768-17778, 1987
A;Title: Cartilage proteoglycan aggregates. The link protein and proteoglycan amino-term
A;Reference number: A28453; MUID:88087071; PMID:3693371
A;Accession: A28453
A;Molecule type: protein
A;Residues: 20-37,'W',39-60,'E',62-64,'X',66-69;70-83;84,89-148,'L',150-238,'S',240,'A',
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF
C;Keywords: glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-2124/Product: proteoglycan core protein #status predicted <MAT>
F;44-135/Domain: immunoglobulin homology <IMM>
F;170-247/Domain: link protein repeat homology <LNK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;504-581/Domain: link protein repeat homology <LNK3>
F;602-683/Domain: link protein repeat homology <LNK4>
F;1914-2034/Domain: C-type lectin homology <LCH>
F;2041-2097/Domain: complement factor H repeat homology <FHD>
F;126,239,333,387,611,667,1842/Binding site: carbohydrate (Asn) (covalent) #status predic

  Query Match             20.6%;  Score 143;  DB 2;  Length 2124;
  Best Local Similarity   32.3%;  Pred. No. 2.4e-06;
  Matches   43;  Conservative   12;  Mismatches   54;  Indels   24;  Gaps    7;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|  ||:    :||: |    ||  ||| | ||    || |: |  |  ||      ||
Db       1913 QCEEGWTKFQGHCYRHFPDRETWVDAERRCREQQ--SHLSSIVTPEEQEFV------NKN 1964

Qy         63 YLTRYIWIGLRVQN-----KGQPCSSISYE----NLVDPF-----ECFMVSRDTRLREWF 108
                | ||||  :      :     |: :|    |  | |     :| ::    |  ||
Db       1965 -AQDYQWIGLNDRTIEGDFRWSDGHSLQFEKWRPNQPDNFFATGEDCVVMIWHER-GEWN 2022

Qy        109 KVDCEQQHSFICK 121
                | |  |  | ||
Db       2023 DVPCNYQLPFTCK 2035


RESULT 28
A55182
aggrecan precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A55182; S55329; S50207; S51355; I78532; I58123
R;Walcz, E.; Deak, F.; Erhardt, P.; Coulter, S.N.; Fueloep, C.; Horvath, P.; Doege, K.J.;
Genomics 22, 364-371, 1994
A;Title: Complete coding sequence, deduced primary structure, chromosomal localization, a
A;Reference number: A55182; MUID:95104847; PMID:7806222
A;Accession: A55182
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-2132 <WAL>
A;Cross-references: UNIPROT:Q61282; GB:L07049; NID:g678541; PIDN:AAC37670.1; PID:g191772
R;Watanabe, H.; Gao, L.; Sugiyama, S.; Doege, K.; Kimata, K.; Yamada, Y.
Biochem. J. 308, 433-440, 1995
A;Title: Mouse aggrecan, a large cartilage proteoglycan: protein sequence, gene structure
A;Reference number: S55329; MUID:95289972; PMID:7772024
A;Accession: S55329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-567,'G',569-1728,'I',1730-2132 <WAT1>
A;Cross-references: GB:U22901; NID:g886014
R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by N
A;Reference number: S50206; MUID:95035091; PMID:7524681
A;Accession: S50207
A;Molecule type: mRNA
A;Residues: 350-481,'R',483-506 <GLU1>
A;Cross-references: EMBL:X80279; NID:g673432
R;Glumoff, V.
submitted to the EMBL Data Library, July 1994
A;Reference number: S51355
A;Accession: S51355
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 350-383,'CPVMSQRERPWAA' <GLU2>
A;Cross-references: EMBL:X80279
R;Watanabe, H.; Kimata, K.; Line, S.; Strong, D.; Gao, L.Y.; Kozak, C.A.; Yamada, Y.
Nature Genet. 7, 154-157, 1994
A;Title: Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in the aggreca
```

```
A;Reference number: I58123; MUID:95004579; PMID:7920633
A;Accession: I78532
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 211-326 <WAT2>
A;Cross-references: GB:S73722; NID:g765215; PIDN:AAB32160.1; PID:g765216
A;Accession: I58123
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 211-240,'MCTASLRRWRVRSFMRHPQRNSPSRRQPTS','AGGWGHAWPPQASSTWPGRAVWTCAALAGW','R
A;Cross-references: GB:S73720; NID:g765211; PIDN:AAB32159.1; PID:g765212
C;Genetics:
A;Map position: 7
A;Introns: 253/1
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: cartilage; extracellular matrix
F;1-19/Domain: signal sequence #status predicted <SIG>
F;44-135/Domain: immunoglobulin homology <IMM>
F;170-247/Domain: link protein repeat homology <LNK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;504-581/Domain: link protein repeat homology <LNK3>
F;602-683/Domain: link protein repeat homology <LNK4>
F;1922-2042/Domain: C-type lectin homology <LCH>
F;2049-2105/Domain: complement factor H repeat homology <FHD>

  Query Match             20.6%;  Score 143;  DB 1;  Length 2132;
  Best Local Similarity   32.3%;  Pred. No. 2.4e-06;
  Matches   43;  Conservative   12;  Mismatches   54;  Indels   24;  Gaps    7;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|  ||:    :||: |    ||  ||| | ||    || |: |  |  ||      ||
Db       1921 QCSEGWTKFQGHCYRHFPDRETWVDAERRCREQQ--SHLSSIVTPEEQEFV------NKN 1972

Qy         63 YLTRYIWIGLRVQN-----KGQPCSSISYE----NLVDPF-----ECFMVSRDTRLREWF 108
                | ||||  :       :     |: :|    |  | |     :| ::    |  ||
Db       1973 -AQDYQWIGLNDRTIEGDFRWSDGHSLQFEKWRPNQPDNFFATGEDCVVMIWHER-GEWN 2030

Qy        109 KVDCEQQHSFICK 121
              | |  |  | ||
Db       2031 DVPCNYQLPFTCK 2043


RESULT 29
S57653
brevican precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57653
R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning and sequence of mouse neurocan and brevican and their different e
A;Reference number: S57653
A;Accession: S57653
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-883 <RAU>
A;Cross-references: UNIPROT:Q61361; EMBL:X87096; NID:g886889; PIDN:CAA60575.1; PID:g8868
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
F;49-138/Domain: immunoglobulin homology <IMM>
F;173-250/Domain: link protein repeat homology <LNK1>
F;271-352/Domain: link protein repeat homology <LNK2>
F;626-657/Domain: EGF homology <EGF>
F;664-784/Domain: C-type lectin homology <LCH>
F;791-847/Domain: complement factor H repeat homology <FHD>

  Query Match             20.5%;  Score 142.5;  DB 2;  Length 883;
  Best Local Similarity   30.6%;  Pred. No. 1e-06;
  Matches   49;  Conservative    8;  Mismatches   50;  Indels   53;  Gaps    8;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              |  || :    ||| |    :|  ||  |  :| | || |: |  |  ||      |  |
Db        664 CSPGWEAFQGACYKHFSTRRSWEEAESQC--RALGAHLTSICTPEEQDFV------NDRY 715

Qy         64 LTRYIWIGLRVQ------------------NKGQPCS-SISYENLVDPFECFMVSRDTR 103
                | ||||  :                  | ||| |  :| || |      ||  |
Db        716 -REYQWIGLNDRTIEGDFLWSDGAPLLYENWNPGQPDSYFLSGENCV-----VMVWHDQ- 768

Qy        104 LREWFKVDCEQQHSFICK----------------FTRPR 126
                :|  | |    |: ||                | |||
Db        769 -GQWSDVPCNYHLSYTCKMGLVSCGPPPQLPLAQIFGRPR 807


RESULT 30
A53210
phospholipase A2 receptor precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A53210
R;Ishizaki, J.; Hanasaki, K.; Higashino, K.; Kishino, J.; Kikuchi, N.; Ohara, O.; Arita,
J. Biol. Chem. 269, 5897-5904, 1994
A;Title: Molecular cloning of pancreatic group I phospholipase A-2 receptor.
A;Reference number: A53210; MUID:94164945; PMID:7509792
A;Accession: A53210
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1463 <ISH>
A;Cross-references: UNIPROT:P49259; GB:D16109; NID:g786165; PIDN:BAA03683.1; PID:g786166
C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II rep
F;178-219/Domain: fibronectin type II repeat homology <2F1>
F;378-501/Domain: C-type lectin homology <LCH>

  Query Match             20.5%;  Score 142.5;  DB 2;  Length 1463;
  Best Local Similarity   26.2%;  Pred. No. 1.8e-06;
  Matches   39;  Conservative   25;  Mismatches   44;  Indels   41;  Gaps    8;

Qy          4 CPSGWSSTDRYCYKPFKQE-----MTWASAERFCSEQAKGGHLLSVETALEASFVDNVLY 58
              || ||   |  |         |  | ||: || |:  || |:::|  :| :|:   |:
Db        959 CPKGWLYFDYKCLLLKIPEGPSDWKNWTSAQDFCVEE--GGTLVAIENEVEQAFITMNLF 1016

Qy         59 ANKEYLTRYIWIGLRVQN-----KGQPCSSISYENLVDPFE-----------------C 95
              :    |  :||||:  :       |:|   :|| |   ||:                 |
Db       1017 GH----TTNVWIGLQDDDYEKWLNGRP---VSYSNW-SPFDTKNIPNHNTTEVQKRIPLC 1068

Qy         96 FMVSRDTRLR---EWFKVDCEQQHSFICK 121
              ::| :       :|:  || : : |:|:
Db       1069 GLLSNNPNFHFTGKWYFEDCREGYGFVCE 1097


RESULT 31
A39086
aggrecan precursor, cartilage long splice form [validated] - human
N;Alternate names: chondroitin sulfate proteoglycan 1; large aggregating proteoglycan; pr
N;Contains: aggrecan cartilage short splice form
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A39086; S50206; A43919; S46659; S66389; S68646; S62786; A34226; B43919; C439
R;Doege, K.J.; Sasaki, M.; Kimura, T.; Yamada, Y.
J. Biol. Chem. 266, 894-902, 1991
A;Title: Complete coding sequence and deduced primary structure of the human cartilage la
A;Reference number: A39086; MUID:91093289; PMID:1985970
A;Accession: A39086
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2162,2201-2329,'A',2392-2415 <DOE>
A;Cross-references: UNIPROT:P16112; GB:M55172; NID:g178258; PIDN:AAA62824.1; PID:g178259
R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by N
A;Reference number: S50206; MUID:95035091; PMID:7524681
A;Accession: S50206
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 350-497 <GLU>
A;Cross-references: EMBL:X80278; NID:g516295
A;Note: this translation is not annotated in GenBank entry HSAGGREC, release 113.0
R;Sandy, J.D.; Flannery, C.R.; Neame, P.J.; Lohmander, L.S.
```

J. Clin. Invest. 89, 1512-1516, 1992
A;Title: The structure of aggrecan fragments in human synovial fluid. Evidence for the i
domain.
A;Reference number: A43919; MUID:92235266; PMID:1569188
A;Accession: A43919
A;Molecule type: protein
A;Residues: 361-370,'X',372-373;393-399,'X',401-407,'X',409 <SAN>
A;Cross-references: PIDN:AAB22079.1; PID:g248844; PIDN:AAB22077.1; PID:g248842; PIDN:AAB
A;Experimental source: synovial fluid
A;Note: sequences modified after extraction from NCBI backbone
R;Barry, F.P.; Neame, P.J.; Sasse, J.; Pearson, D.
Matrix Biol. 14, 323-328, 1994
A;Title: Length variation in the keratan sulfate domain of mammalian aggrecan.
A;Reference number: I46998; MUID:95128522; PMID:7827755
A;Accession: S46659
A;Molecule type: DNA
A;Residues: 764-765,'A',767-846,'V',848-862,'X',864 <BAR>
A;Cross-references: EMBL:S74659; NID:g807127; PIDN:AAC60643.1; PID:g807128
A;Note: the authors translated the codon GAA for residue 803 as Ala and CYT for residue
R;Ilic, M.Z.; Mok, M.T.; Williamson, O.D.; Campbell, M.A.; Hughes, C.E.; Handley, C.J.
Arch. Biochem. Biophys. 322, 22-30, 1995
A;Title: Catabolism of aggrecan by explant cultures of human articular cartilage in the
A;Reference number: S66389; MUID:96004775; PMID:7574678
A;Accession: S66389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 17-23;24,'X',26-27;393-401;402-403 <ILI>
R;Fosang, A.J.; Last, K.; Knaeuper, V.; Murphy, G.; Neame, P.J.
FEBS Lett. 380, 17-20, 1996
A;Title: Degradation of cartilage aggrecan by collagenase-3 (MMP-13).
A;Reference number: S68646; MUID:96181659; PMID:8603731
A;Accession: S68646
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'V',404-405,'XX' <FOS>
R;Dudhia, J.; Davidson, C.M.; Wells, T.M.; Vynios, D.H.; Hardingham, T.E.; Bayliss, M.T.
Biochem. J. 313, 933-940, 1996
A;Title: Age-related changes in the content of the C-terminal region of aggrecan in huma
A;Reference number: S62786; MUID:96190740; PMID:8611178
A;Accession: S62786
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1778-1927,'A',1929-1963,'V',1965-2162,2201-2415 <DUD>
A;Cross-references: EMBL:X17406; NID:g30248; PIDN:CAA35463.1; PID:g30249
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1990
R;Baldwin, C.T.; Reginato, A.M.; Prockop, D.J.
J. Biol. Chem. 264, 15747-15750, 1989
A;Title: A new epidermal growth factor-like domain in the human core protein for the lar
A;Reference number: A34226; MUID:89380154; PMID:2789216
A;Accession: A34226
A;Molecule type: mRNA
A;Residues: 1936-1963,'V',1965-2069,'A',2071-2415 <BAL>
A;Cross-references: GB:J05062; NID:g181167; PIDN:AAA35726.1; PID:g181168
C;Genetics:
A;Gene: GDB:AGC1; CSPG1; CSPGCP; MSK16
A;Cross-references: GDB:127479; OMIM:155760
A;Map position: 15q26-15q26
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: alternative splicing; cartilage; chondroitin sulfate proteoglycan; extracell
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-2415/Product: aggrecan cartilage long splice form #status predicted <MATL>
F;20-2162,2201-2415/Product: aggrecan cartilage short splice form #status predicted <MAT
F;20-2162,2201-2329,'A',2392-2415/Product: aggrecan short splice form #status predicted
F;44-135/Domain: immunoglobulin homology <IMM>
F;170-247/Domain: link protein repeat homology <LNK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;495-572/Domain: link protein repeat homology <LNK3>
F;593-673/Domain: link protein repeat homology <LNK4>
F;677-861/Domain: keratan sulfate attachment #status predicted <KSA>
F;864-1510/Domain: chondroitin sulfate attachment #status predicted <CS1>
F;1511-2162/Domain: chondroitin sulfate attachment #status predicted <CS2>
F;2168-2198/Domain: EGF homology <EGF>
F;2205-2325/Domain: C-type lectin homology <LCH>
F;2332-2388/Domain: complement factor H repeat homology <FHD>
F;126,239,333,387,434,602,657,737,1898/Binding site: carbohydrate (Asn) (covalent) #statu
F;371,376/Binding site: keratan sulfate (Thr) (covalent) #status predicted

Query Match 20.4%; Score 142; DB 1; Length 2415;
Best Local Similarity 31.3%; Pred. No. 3.5e-06;
Matches 42; Conservative 11; Mismatches 53; Indels 28; Gaps 7;

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Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              |  ||:    :||: |     ||  ||| | ||     || |: |   |  ||:|    | :
Db       2205 CEEGWNKYQGHCYRHFPDRETWVDAERRCREQQ--SHLSSIVTPEEQEFVNN----NAQ- 2257

Qy         64 LTRYIWIGLRVQ--------NKGQPCSSISYENL--VDPFECFMVSRDTRLR------EW 107
                | ||||  :         : | |   : :||     |   |     |  :       ||
Db       2258 --DYQWIGLNDRTIEGDFRWSDGHP---MQFENWRPNQPDNFFAAGEDCVVMIWHEKGEW 2312

Qy        108 FKVDCEQQHSFICK 121
              | |     | ||
Db       2313 NDVPCNYHLPFTCK 2326
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RESULT 32
T46256
brevican - human (fragment)
N;Alternate names: protein DKFZp761L191.1
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46256
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23031
A;Accession: T46256
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-330 <AAA>
A;Cross-references: UNIPROT:Q9NT67; EMBL:AL137504
A;Experimental source: adult amygdala; clone DKFZp761L191
C;Genetics:
A;Note: DKFZp761L191.1
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGI

Query Match 20.4%; Score 141.5; DB 2; Length 330;
Best Local Similarity 28.8%; Pred. No. 4.3e-07;
Matches 46; Conservative 10; Mismatches 51; Indels 53; Gaps 7;

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Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              |  || :    ||| |    :|  ||  |  :  | || |: |   |  |::|
Db        107 CNPGWDAFQGACYKHFSTRRSWEEAETQC--RMYGAHLASISTPEEQDFINN-------R 157

Qy         64 LTRYIWIGLRVQ------------------NKGQPCS-SISYENLVDPFECFMVSRDTR 103
                | ||||  :                  | ||| |  :| || |       ||  |
Db        158 YREYQWIGLNDRTIEGDFLWSDGVPLLYENWNPGQPDSYFLSGENCV-----VMVWHDQ- 211

Qy        104 LREWFKVDCEQQHSFICK----------------FTRPR 126
              :|  | |    |: ||                | |||
Db        212 -GQWSDVPCNYHLSYTCKMGLVSCGPPPELPLAQVFGRPR 250
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RESULT 33
S49126
brevican precursor - rat
N;Alternate names: aggrecan-like protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S49126; I55457
R;Seidenbecher, C.I.; Langnase, K.; Wax, H.; Seidel, B.; Garner, C.C.; Gundelfinger, E.D
submitted to the EMBL Data Library, June 1994
A;Description: Molecular cloning of a new member of the aggrecan/versican family of prote
A;Reference number: S49126
A;Accession: S49126
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-883 <SEI>

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A;Cross-references: UNIPROT:P55068; EMBL:X79881; NID:g509396; PIDN:CAA56255.1; PID:g5093
R;Seidenbecher, I.C.; Richter, K.; Rauch, U.; Fassler, R.; Garner, C.C.; Gundelfinger, E
J. Biol. Chem. 270, 27206-27212, 1995
A;Title: Brevican, a Chondroitin Sulfate Proteoglycan of Rat Brain, Occurs as Secreted a
A;Reference number: I55457; MUID:96070828; PMID:7592978
A;Accession: I55457
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-883 <RES>
A;Cross-references: EMBL:X79881; NID:g509396; PIDN:CAA56255.1; PID:g509397
C;Comment: For an alternative splice form, see PIR:A53908.
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: alternative splicing
F;49-138/Domain: immunoglobulin homology <IMM>
F;173-250/Domain: link protein repeat homology <LNK1>
F;271-352/Domain: link protein repeat homology <LNK2>
F;626-657/Domain: EGF homology <EGF>
F;664-784/Domain: C-type lectin homology <LCH>
F;791-847/Domain: complement factor H repeat homology <FHD>

  Query Match             20.2%;  Score 140.5;  DB 2;  Length 883;
  Best Local Similarity   30.6%;  Pred. No. 1.6e-06;
  Matches   49;  Conservative    7;  Mismatches   51;  Indels   53;  Gaps    8;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              |  ||      ||| |    :|  ||  |  :| | || |: |  |  ||      |  |
Db        664 CSPGWEPFQGACYKHFSTRRSWEEAESQC--RALGAHLTSICTPEEQDFV------NDRY 715

Qy         64 LTRYIWIGLRVQ-------------------NKGQPCS-SISYENLVDPFECFMVSRDTR 103
                 | ||||  :                   | ||| |  :| || |      ||  |
Db        716 -REYQWIGLNDRTIEGDFLWSDGPPLLYENWNPGQPDSYFLSGENCV-----VMVWHDQ- 768

Qy        104 LREWFKVDCEQQHSFICK-----------------FTRPR 126
                :|  | |    |: ||                 | |||
Db        769 -GQWSDVPCNYHLSYTCKMGLVSCGPPPQLPLAQIFGRPR 807


RESULT 34
A38609
lectin, galactose-specific - western diamondback rattlesnake
C;Species: Crotalus atrox (western diamondback rattlesnake)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 09-Jul-2004
C;Accession: A38609
R;Hirabayashi, J.; Kusunoki, T.; Kasai, K.
J. Biol. Chem. 266, 2320-2326, 1991
A;Title: Complete primary structure of a galactose-specific lectin from the venom of the
A;Reference number: A38609; MUID:91115849; PMID:1989986
A;Accession: A38609
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-135 <HIR>
A;Cross-references: UNIPROT:P21963
C;Superfamily: tetranectin; C-type lectin homology
F;3-131/Domain: C-type lectin homology <LCH>
F;3-14,31-131,106-123/Disulfide bonds: #status predicted

  Query Match             20.1%;  Score 140;  DB 2;  Length 135;
  Best Local Similarity   28.5%;  Pred. No. 2.3e-07;
  Matches   39;  Conservative   21;  Mismatches   51;  Indels   26;  Gaps    6;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              ||  |    :  ||| | |  ||  || || :   | || |     |: :         ||
Db          3 CPLDWLPMNGLCYKIFNQLKTWEDAEMFCRKYKPGCHLASFHRYGESLEI-------AEY 55

Qy         64 LTRY------IWIGLRVQNK-------GQPCSS-ISYE-NLVDPFE----CFMVSRDTRL 104
              :: |       :|||| : |       : |:  :::: |  | ::    |  :    |
Db         56 ISDYHKGQENVWIGLRDKKKDFSWEWTDRSCTDYLTWDKNQPDHYQNKEFCVELVSLTGY 115

Qy        105 REWFKVDCEQQHSFICK 121
              | |    || : :|:|:
Db        116 RLWNDQVCESKDAFLCQ 132


RESULT 35
LNRC1
lectin BRA3-1 precursor - barnacle (Megabalanus rosa)
C;Species: Megabalanus rosa
C;Date: 24-Feb-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: JC1503; A26094
R;Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, T.
Gene 128, 251-255, 1993
A;Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure and
A;Reference number: JC1503; MUID:93292994; PMID:8514190
A;Accession: JC1503
A;Molecule type: DNA; mRNA
A;Residues: 1-162 <TAK>
A;Cross-references: UNIPROT:Q25459; DDBJ:D13299
R;Muramoto, K.; Kamiya, H.
Biochim. Biophys. Acta 874, 285-295, 1986
A;Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.
A;Reference number: A26094
A;Accession: A26094
A;Molecule type: protein
A;Residues: 25-145,'K',147-162 <MUR>
A;Note: 146-Arg was also found
C;Comment: This galactose-binding lectin is isolated from the coelomic fluid.
C;Comment: This protein plays important roles in defense mechanisms and in development ar
C;Comment: The molecule is a tetramer of identical chains.
C;Genetics:
A;Introns: 22/1; 47/2; 86/3
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemolymph; homotetramer; lectin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-162/Product: lectin BRA3-1 #status experimental <MAT>
F;26-150/Domain: C-type lectin homology <LCH>
F;26-39,56-150,125-142/Disulfide bonds: #status experimental
F;157/Disulfide bonds: interchain (to 160) #status experimental
F;160/Disulfide bonds: interchain (to 157) #status experimental

  Query Match             20.1%;  Score 140;  DB 1;  Length 162;
  Best Local Similarity   24.8%;  Pred. No. 2.8e-07;
  Matches   33;  Conservative   27;  Mismatches   51;  Indels   22;  Gaps    5;

Qy          4 CPSG--WSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              ||    |   | :||     :: |  |:  |     | :| :::: || :|:   :  |:
Db         26 CPGNLDWQEYDGHCYWASTYQVRWNDAQLACQTVHPGAYLATIQSQLENAFISETVSNNR 85

Qy         62 EYLTRYIWIGLR--------VQNKGQPCSSISYENLVDP-----FECFMVSRDTRLREWF 108
                    :||||         | : |:  :  :| :  :|       :| :|: ||   :|
Db         86 ------LWIGLNDIDLEGHYVWSNGE-ATDFTYWSSNNPNNWENQDCGVVNYDTVTGQWD 138

Qy        109 KVDCEQQHSFICK 121
                 || :  :|:||
Db        139 DDDCNKNRNFLCK 151


RESULT 36
S54979
pancreatitis-associated protein PAP-3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: S54979; S43438
R;Dusetti, N.J.; Frigerio, J.M.; Szpirer, C.; Dagorn, J.C.; Iovanna, J.L.
Biochem. J. 307, 9-16, 1995
A;Title: Cloning, expression and chromosomal localization of the rat pancreatitis-associa
A;Reference number: S54979; MUID:95234061; PMID:7717998
A;Accession: S54979
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-174 <DUS>
A;Cross-references: UNIPROT:P42854; EMBL:U09193; NID:g483931; PIDN:AAA79231.1; PID:g48393
R;Frigerio, J.M.; Dusetti, N.J.; Garrido, P.; Dagorn, J.C.; Iovanna, J.L.
Biochim. Biophys. Acta 1216, 329-331, 1993
A;Title: The pancreatitis associated protein III (PAP III), a new member of the PAP gene
A;Reference number: S43438; MUID:94060113; PMID:8241280
A;Accession: S43438
```

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-174 <FRI>
A;Cross-references: GB:L20869; GB:S67496; NID:g463279; PIDN:AAA41809.1; PID:g463280
C;Genetics:
A;Introns: 26/1; 65/3; 111/3; 153/1
C;Superfamily: tetranectin; C-type lectin homology
F;40-170/Domain: C-type lectin homology <LCH>

Query Match 20.1%; Score 140; DB 2; Length 174;
Best Local Similarity 25.5%; Pred. No. 3e-07;
Matches 35; Conservative 26; Mismatches 58; Indels 18; Gaps 3;

Qy 2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
Db 38 ISCPKGSRAYGSYCYALFSVSKSWFDADLAC-QKRPSGHLVSVLSGSEASFVSSLIKSSG 96

Qy 62 EYLTRYIWIGLRVQNKGQPCSSISYE----------NLVDPFECFMVSRDTRLR 105
Db 97 N-SGQNVWIGLHDPTLGQEPNRGGWEWSNADVMNYFNWETNPSSVSGSHCGTLTRASGFL 155

Qy 106 EWFKVDCEQQHSFICKF 122
Db 156 RWRENNCISELPYVCKF 172

RESULT 37
B56829
alboaggregin-B alpha chain - green pit viper (fragment)
C;Species: Trimeresurus albolabris (green pit viper)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: B56829
R;Yoshida, E.; Fujimura, Y.; Miura, S.; Sugimoto, M.; Fukui, H.; Narita, N.; Usami, Y.;
Biochem. Biophys. Res. Commun. 191, 1386-1392, 1993
A;Title: Alboaggregin-B and botrocetin, two snake venom proteins with highly homologous
A;Reference number: A56829; MUID:93221514; PMID:8466514
A;Accession: B56829
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-40 <YOS>
A;Cross-references: UNIPROT:Q9PS19
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:128751)
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer

Query Match 20.0%; Score 139; DB 2; Length 40;
Best Local Similarity 57.5%; Pred. No. 7.4e-08;
Matches 23; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLL 42
Db 1 DCPSDWSSFKQYCYQIIKQLKTWEDAERFCMDQVKGAHLV 40

RESULT 38
LNRC3
lectin BRA3-2 precursor - barnacle (Megabalanus rosa)
C;Species: Megabalanus rosa
C;Date: 31-Dec-1988 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: JC1504; A26094
R;Takamatsu, N.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, T.
Gene 128, 251-255, 1993
A;Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure an
A;Reference number: JC1503; MUID:93292994; PMID:8514190
A;Accession: JC1504
A;Molecule type: mRNA
A;Residues: 1-162 <TAK>
A;Cross-references: UNIPROT:Q25459
R;Muramoto, K.; Kamiya, H.
Biochim. Biophys. Acta 874, 285-295, 1986
A;Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.
A;Reference number: A26094
A;Accession: A26094
A;Molecule type: protein
A;Residues: 25-162 <MUR>
A;Note: 146-Arg was also found
C;Comment: This three galactose-binding lectin is isolated from the coelomic fluid.
C;Comment: This protein plays important roles in defense mechanisms and in development ar
C;Comment: The molecule is a tetramer of identical chains.
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemolymph; homotetramer; lectin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-162/Product: lectin BRA3-2 #status experimental <MAT>
F;26-150/Domain: C-type lectin homology <LCH>
F;26-39,56-150,125-142/Disulfide bonds: #status experimental
F;157/Disulfide bonds: interchain (to 160) #status experimental
F;160/Disulfide bonds: interchain (to 157) #status experimental

Query Match 20.0%; Score 139; DB 1; Length 162;
Best Local Similarity 24.8%; Pred. No. 3.5e-07;
Matches 33; Conservative 27; Mismatches 51; Indels 22; Gaps 5;

Qy 4 CPSG--WSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
Db 26 CPGNLDWQEYDGHCYWASTYQVRWNDAQLACQTVHPGAYLATIQSQLENAFISETVSNNR 85

Qy 62 EYLTRYIWIGLR--------VQNKGQPCSSISYENLVDP-----FECFMVSRDTRLREWF 108
Db 86 ------LWIGLNDIDLEGHYVWSNGE-ATDFTYWSSNNPNNWENQDCGVVNYDTVTGQWD 138

Qy 109 KVDCEQQHSFICK 121
Db 139 DDDCNKNKNFLCK 151

RESULT 39
A39808
proteoglycan core protein, cartilage - bovine (fragments)
N;Alternate names: aggrecan; aggregating cartilage proteoglycan
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Mar-1992 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A34234; A27752; A39808; A27751; E29164; B27751; C27751; D27751; E27751; F27
R;Antonsson, P.; Heinegard, D.; Oldberg, A.
J. Biol. Chem. 264, 16170-16173, 1989
A;Title: The keratan sulfate-enriched region of bovine cartilage proteoglycan consists of
A;Reference number: A34234; MUID:89380219; PMID:2528543
A;Accession: A34234
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 128-621 <ANT>
A;Cross-references: UNIPROT:P13608; GB:J05028
R;Oldberg, A.; Antonsson, P.; Heinegard, D.
Biochem. J. 243, 255-259, 1987
A;Title: The partial amino acid sequence of bovine cartilage proteoglycan,deduced from a
A;Reference number: A27752; MUID:87270630; PMID:3111460
A;Accession: A27752
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 622-1340 <OLD>
R;Sandy, J.D.; Boynton, R.E.; Flannery, C.R.
J. Biol. Chem. 266, 8198-8205, 1991
A;Title: Analysis of the catabolism of aggrecan in cartilage explants by quantitation of
A;Reference number: A39808; MUID:91217051; PMID:2022637
A;Accession: A39808
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28;59-82;131-137,'QSET',142-149;196-207;226-249;1137-1143;1252-1267;1274-12
R;Perin, J.P.; Bonnet, F.; Jolles, P.
FEBS Lett. 206, 73-77, 1986
A;Title: Structural relationship between link proteins and proteoglycan monomers.
A;Reference number: A27751; MUID:87005253; PMID:3530809
A;Accession: A27751
A;Molecule type: protein
A;Residues: 29-58;74-130;174-175,'A',177-204;208-225 <PER>
R;Perin, J.P.; Bonnet, F.; Jolles, J.; Jolles, P.

```
FEBS Lett. 176, 37-42, 1984
A;Title: Sequence data concerning the protein core of the cartilage proteoglycan monomer
A;Reference number: A91327; MUID:85027710; PMID:6489519
A;Accession: E29164
A;Molecule type: protein
A;Residues: 1230-1249 <PE2>
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: glycoprotein
F;8-28/Domain: link protein repeat homology (fragment) <LNK1>
F;29-58/Domain: link protein repeat homology (fragment) <LNK2>
F;80-146/Domain: link protein repeat homology (fragments) <LNK3>
F;167-248/Domain: link protein repeat homology <LNK4>
F;1130-1250/Domain: C-type lectin homology <LCH>
F;1257-1313/Domain: complement factor H repeat homology <FHD>

  Query Match             19.9%;  Score 138;  DB 2;  Length 1340;
  Best Local Similarity   30.5%;  Pred. No. 4.7e-06;
  Matches   40;  Conservative   12;  Mismatches   57;  Indels   22;  Gaps    6;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              |  ||:    :||: |    ||  ||  | :|    || |: |  |  ||:|    | :
Db       1130 CEEGWTKFQGHCYRHFPDRATWVDAESQCRKQQ--SHLSSIVTPEEQEFVNN----NAQ- 1182

Qy         64 LTRYIWIGLRVQN-----KGQPCSSISYENL--VDPFECFMVSRDTRLR------EWFKV 110
                | ||||  :      :     |: :||     |   |    |  :       ||  |
Db       1183 --DYQWIGLNDKTIEGDFRWSDGHSLQFENWRPNQPDNFFATGEDCVVMIWHEKGEWNDV 1240

Qy        111 DCEQQHSFICK 121
              |  |  | ||
Db       1241 PCNYQLPFTCK 1251


RESULT 40
S48719
phospholipase-A(2) receptor protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S48719
R;Higashino, K.; Ishizaki, J.; Kishino, J.; Ohara, O.; Arita, H.
Eur. J. Biochem. 225, 375-382, 1994
A;Title: Structural comparison of phospholipase-A(2)-binding regions in phospholipase-A(
A;Reference number: S48719; MUID:95010128; PMID:7925459
A;Accession: S48719
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1487 <HIG>
A;Cross-references: UNIPROT:Q62028; GB:D30779; NID:g1375042; PIDN:BAA06443.1; PID:g69175
C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
F;181-222/Domain: fibronectin type II repeat homology <2F1>
F;380-503/Domain: C-type lectin homology <LCH>

  Query Match             19.9%;  Score 138;  DB 2;  Length 1487;
  Best Local Similarity   26.7%;  Pred. No. 5.3e-06;
  Matches   39;  Conservative   31;  Mismatches   42;  Indels   34;  Gaps    9;

Qy          4 CPSGWSSTDRYCY-----KPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLY 58
              || ||    :  |:     |  ::  ||  |: ||   |||| |:|::: || :|:   |:
Db        957 CPKGWLYFNYKCFLVTIPKDPRELKTWTGAQEFC--VAKGGTLVSIKSELEQAFITMNLF 1014

Qy         59 ANKEYLTRYIWIGLRVQN-----KGQPC--SSISYENLVD-------PFE-----CFMVS 99
                 |  :||||:  |       |:|   |: |  ::::         |:     | ::|
Db        1015 GQ----TTNVWIGLQSTNHEKWVNGKPLVYSNWSPSDIINIPSYNTTEFQKHIPLCALMS 1070

Qy        100 RDTRLR---EWFKVDC-EQQHSFICK 121
               :       :|:  || :: : |:|:
Db        1071 SNPNFHFTGKWYFDDCGKEGYGFVCE 1096


RESULT 41
T42630
aggrecan - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42630
R;Hering, T.M.; Kollar, J.; Huynh, T.D.
submitted to the EMBL Data Library, September 1996
A;Description: Complete coding sequence of bovine aggrecan: comparative structural analys
A;Reference number: Z22182
A;Accession: T42630
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2327 <HER>
A;Cross-references: UNIPROT:P13608; EMBL:U76615; NID:g1730259; PID:g1730260; PIDN:AAB3852
A;Experimental source: articular chondrocytes
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF
C;Keywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycoprote

  Query Match             19.9%;  Score 138;  DB 2;  Length 2327;
  Best Local Similarity   30.5%;  Pred. No. 8.8e-06;
  Matches   40;  Conservative   12;  Mismatches   57;  Indels   22;  Gaps    6;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              |  ||:    :||: |    ||  ||  | :|    || |: |  |  ||:|    | :
Db       2117 CEEGWTKFQGHCYRHFPDRATWVDAESQCRKQQ--SHLSSIVTPEEQEFVNN----NAQ- 2169

Qy         64 LTRYIWIGLRVQN-----KGQPCSSISYENL--VDPFECFMVSRDTRLR------EWFKV 110
                | ||||  :      :     |: :||     |   |    |  :       ||  |
Db       2170 --DYQWIGLNDKTIEGDFRWSDGHSLQFENWRPNQPDNFFATGEDCVVMIWHEKGEWNDV 2227

Qy        111 DCEQQHSFICK 121
              |  |  | ||
Db       2228 PCNYQLPFTCK 2238


RESULT 42
S78596
ovocleidin - chicken
C;Species: Gallus gallus (chicken)
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 20-Sep-1999
C;Accession: S78596
R;Baernholdt, D.; Andersen, S.O.
submitted to the Protein Sequence Database, September 1998
A;Reference number: S78596
A;Accession: S78596
A;Molecule type: protein
A;Residues: 1-142 <BAE>
A;Experimental source: egg-shell
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: phosphoprotein
F;5-16,33-138,113-130/Disulfide bonds: #status experimental
F;61,67/Binding site: phosphate (Ser) (covalent) #status experimental

  Query Match             19.6%;  Score 136.5;  DB 2;  Length 142;
  Best Local Similarity   25.0%;  Pred. No. 5.6e-07;
  Matches   35;  Conservative   21;  Mismatches   57;  Indels   27;  Gaps    4;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK-- 61
              |  ||  |   |    | :|::|: || ||      | || :| :| |   :  :| |::
Db          5 CGPGWVPTPGGCLGFFSRELSWSRAESFCRRWGPGSHLAAVRSAAELRLLAELLNASRGG 64

Qy         62 ----EYLTRYIWIGLRVQNKGQPCSSISY---ENLVDPF-------------ECFMVSRD 101
                   |     :||||      :|  | |:   :     |               |  :  :
Db         65 DGSGEGADGRVWIGLH-----RPAGSRSWRWSDGTAPRFASWHRTAKARRGGRCAALRDE 119

Qy        102 TRLREWFKVDCEQQHSFICK 121
                    |   | ::::|:||
Db        120 EAFTSWAARPCTERNAFVCK 139


RESULT 43
T29536
hypothetical protein T19E7.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29536
R;Pauley, A.; Gattung, S.
```

submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid T19E7.
A;Reference number: Z20637
A;Accession: T29536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-178 <PAU>
A;Cross-references: UNIPROT:Q22591; EMBL:U42843; PIDN:AAA83595.1; CESP:T19E7.1
C;Genetics:
A;Gene: CESP:T19E7.1
A;Introns: 52/3; 103/1

Query Match 19.2%; Score 133.5; DB 2; Length 178;
Best Local Similarity 28.9%; Pred. No. 1.5e-06;
Matches 39; Conservative 15; Mismatches 58; Indels 23; Gaps 6;

```
Qy          6 SGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEYLT 65
              |||   : : || |: :: |  ||  |  :: ||||:|::   |  ||  :   |
Db         52 SGWQLYEDHWYKMFETDVMWIPAENVC--RSMGGHLVSIKDESENLFVHKLRKKNN---- 105

Qy         66 RYIWIGLRVQN------KGQPCSSISYENLV--DPFE-----CFMVSRDTRLREWFKVDC 112
                |||||   |      |    |   | |    | |      :|     :   ||   |
Db        106 --IWIGLNKLNDTFHVYKWSDGSEADYLNWASSQPNEPDVDCAYMAFHQEQRGTWFDYGC 163

Qy        113 EQQ--HSFICKFTRP 125
               :     |:||   |
Db        164 REMLPQFFVCKLPMP 178
```

RESULT 44
T30273
hypothetical protein - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30273
R;Moy, G.W.; Mendoza, L.M.; Schulz, J.R.; Swanson, W.J.; Glabe, C.G.; Vacquier, V.D.
J. Cell Biol. 133, 809-817, 1996
A;Title: The sea urchin sperm receptor for egg jelly is a modular protein with extensive
A;Reference number: Z20802; MUID:96234669; PMID:8666666
A;Accession: T30273
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1450 <MOY>
A;Cross-references: UNIPROT:Q26627; EMBL:U40832; NID:g1353652; PID:g1353653; PIDN:AAB084
C;Genetics:
A;Note: REJ

Query Match 19.1%; Score 132.5; DB 2; Length 1450;
Best Local Similarity 29.8%; Pred. No. 1.9e-05;
Matches 36; Conservative 16; Mismatches 50; Indels 19; Gaps 5;

```
Qy         14 YCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEYLTRYIWIGLR 73
              |||   : :  |  |   | :| :|  | |: :| | :||    ||    : || ||||
Db         80 YCYLWERVDYNWTQARESCIDQGRGAELASIHSAEENAFV----YAQ---IRRYAWIGLS 132

Qy         74 VQ--------NKGQPCSSISY---ENLVDPFECFMVSRDTRLREWFKVDCEQQHSFICKF 122
               |          | |   :|:      :  :|  | :  |:  |  :||    : |||
Db        133 DQVTEGVFDYADGTPVDYLSFPDKNKQSETRDCVYV-KHLRVDNWSLLDCRANKTSICKS 191

Qy        123 T 123
               |
Db        192 T 192
```

RESULT 45
I50421
aggrecan precursor - chicken
N;Alternate names: cartilage chondroitin sulfate proteoglycan core protein
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I50421; S39796; S27356; A25442; A32002; I50216; A37072; B37072
R;Li, H.; Schwartz, N.B.; Vertel, B.M.
J. Biol. Chem. 268, 23504-23511, 1993
A;Title: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and
A;Reference number: A48884; MUID:94043149; PMID:8226878
A;Accession: I50421
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2109 <LIX>
A;Cross-references: UNIPROT:P07898; GB:L21913; NID:g416133; PIDN:AAB19128.1; PID:g416134
R;Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 296, 885-887, 1993
A;Reference number: S39796; MUID:94107258; PMID:8280087
A;Contents: annotation; erratum
A;Accession: S39796
A;Molecule type: mRNA
A;Residues: 1-361,'DL',364-600,'R',602-999,'R',1001-1028,'P',1030-1250,'D',1252-1602,'A',
A;Cross-references: GB:M88101
R;Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 288, 903-910, 1992
A;Title: Molecular cloning of chicken aggrecan. Structural analyses.
A;Reference number: S27356; MUID:93111968; PMID:1339285
A;Accession: S27356
A;Molecule type: mRNA
A;Residues: 1-361,'DL',364-600,'R',602-999,'R',1001-1028,'P',1030-1250,'D',1252-1549,'T',
A;Cross-references: EMBL:M88101
R;Sai, S.; Tanaka, T.; Kosher, R.A.; Tanzer, M.L.
Proc. Natl. Acad. Sci. U.S.A. 83, 5081-5085, 1986
A;Title: Cloning and sequence analysis of a partial cDNA for chicken cartilage proteoglyc
A;Reference number: A25442; MUID:86259736; PMID:3460082
A;Accession: A25442
A;Molecule type: mRNA
A;Residues: 1693-1795,'G',1797-1855,1894-2109 <SAI>
A;Cross-references: GB:M13993; NID:g211654; PIDN:AAA48720.1; PID:g211655
A;Experimental source: sternal cartilage
R;Tanaka, T.; Har-El, R.; Tanzer, M.L.
J. Biol. Chem. 263, 15831-15835, 1988
A;Title: Partial structure of the gene for chicken cartilage proteoglycan core protein.
A;Reference number: A32002; MUID:89008500; PMID:3170613
A;Accession: A32002
A;Molecule type: DNA
A;Residues: 1893-1987,'S',1989-2022 <TAN>
A;Note: the authors translated the codon TCC for residue 1787 as Phe
R;Krueger, R.C.
J. Biol. Chem. 265, 12088-12097, 1990
A;Title: Chick cartilage chondroitin sulfate proteoglycan core protein: II. Nucleotide se
A;Reference number: I50216; MUID:90307744; PMID:1694853
A;Accession: I50216
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'PA',1044-1559 <KRU>
A;Cross-references: GB:M38187; NID:g211685; PIDN:AAA48731.1; PID:g555441
R;Krueger Jr., R.C.; Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.
J. Biol. Chem. 265, 12075-12087, 1990
A;Title: Chick cartilage chondroitin sulfate proteoglycan core protein. I. Generation and
A;Reference number: A37072; MUID:90307743; PMID:2365711
A;Accession: A37072
A;Molecule type: protein
A;Residues: 998-1015,'X',1017-1019,'X',1021-1023 <KR2>
A;Note: amino end of 86K core peptide CS-A
A;Accession: B37072
A;Molecule type: protein
A;Residues: 1247-1250,'D',1252-1272,'X',1274-1275 <KR3>
A;Note: amino end of 75K core peptide CS-B
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF
C;Keywords: alternative splicing
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-2109/Product: aggrecan #status predicted <MAT>
F;44-131/Domain: immunoglobulin homology <IMM>
F;166-243/Domain: link protein repeat homology <LNK1>
F;264-346/Domain: link protein repeat homology <LNK2>
F;537-614/Domain: link protein repeat homology <LNK3>
F;635-716/Domain: link protein repeat homology <LNK4>
F;1859-1890/Domain: EGF homology <EGF>
F;1897-2017/Domain: C-type lectin homology <LCH>
F;2024-2080/Domain: complement factor H repeat homology <FHD>

Query Match 19.0%; Score 132; DB 1; Length 2109;
Best Local Similarity 29.8%; Pred. No. 3.3e-05;
Matches 39; Conservative 13; Mismatches 57; Indels 22; Gaps 6;

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Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              |  ||     :||: |::  ||  ||  | |      || |: |  |  ||::       :
Db       1897 CEEGWIKFQGHCYRHFEERETWMDAESRCREHQ--AHLSSIITPEEQEFVNS-------H 1947

Qy         64 LTRYIWIGL---RVQN--KGQPCSSISYENL--VDPFECFMVSRDTRLR------EWFKV 110
                | ||||    |:|  :     |: :||     |   |     |  :          || |
Db       1948 AQDYQWIGLSDRAVENDFRWSDGHSLQFENWRPNQPDNFFFAGEDCVVMIWHEQGEWNDV 2007

Qy        111 DCEQQHSFICK 121
                |     | ||
Db       2008 PCNYHLPFTCK 2018
```

RESULT 46
S52781
neurocan - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52781
R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
submitted to the EMBL Data Library, February 1995
A;Description: Amino acid sequence of mouse neurocan and brevican and their different ex
A;Reference number: S52781
A;Accession: S52781
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1268 <RAU>
A;Cross-references: UNIPROT:P55066; EMBL:X84727; NID:g758629; PIDN:CAA59216.1; PID:g7586
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
F;176-253/Domain: link protein repeat homology <LNK1>
F;274-355/Domain: link protein repeat homology <LNK2>
F;964-995/Domain: EGF homology <EGF>
F;1040-1160/Domain: C-type lectin homology <LCH>
F;1167-1223/Domain: complement factor H repeat homology <FHD>

Query Match 18.8%; Score 131; DB 2; Length 1268;
Best Local Similarity 28.3%; Pred. No. 2.4e-05;
Matches 39; Conservative 15; Mismatches 48; Indels 36; Gaps 8;

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Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              |  ||     :||: |     |  ||| |  :|  ||| || :  |  |:::  : |
Db       1040 CDRGWHKFQGHCYRYFAHRRAWEDAERDCRRRA--GHLTSVHSPEEHKFINSFGHENS-- 1095

Qy         64 LTRYIWIGLR----------VQNKGQPCSSISYEN----LVDPF-----EC-FMVSRDTR 103
                  ||||              | |     : |||      | |     :|  ||: ::
Db       1096 -----WIGLNDRTVERDFQWTDNTG-----LQYENWREKQPDNFFAGGEDCVVMVAHES- 1144

Qy        104 LREWFKVDCEQQHSFICK 121
                |  | |     ::||
Db       1145 -GRWNDVPCNYNLPYVCK 1161
```

RESULT 47
A26697
echinoidin - sea urchin (Anthocidaris crassispina)
C;Species: Anthocidaris crassispina
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C;Accession: A26697
R;Giga, Y.; Ikai, A.; Takahashi, K.
J. Biol. Chem. 262, 6197-6203, 1987
A;Title: The complete amino acid sequence of echinoidin, a lectin from the coelomic flui
A;Reference number: A26697; MUID:87194838; PMID:3571253
A;Accession: A26697
A;Molecule type: protein
A;Residues: 1-147 <GIG>
A;Cross-references: UNIPROT:P06027
C;Superfamily: tetranectin; C-type lectin homology
F;3-141/Domain: C-type lectin homology <LCH>
F;3-14,31-141,116-132/Disulfide bonds: #status predicted

Query Match 18.7%; Score 130; DB 2; Length 147;
Best Local Similarity 26.2%; Pred. No. 2.8e-06;
Matches 37; Conservative 24; Mismatches 56; Indels 24; Gaps 7;

```
Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFC---SEQAKG-----GHLLSVETALEASFVDN 55
              ||: |:|    ||: |   :|||  |:||   |  ::|      |||:|: :  | :|| :
Db          3 CPTFWTSFGSNCYRFFAVSLTWAEGEQFCQSFSVPSRGDIDSIGHLVSIHSETEQNFVYH 62

Qy         56 VL-YANKEYLTRYIWIGLRVQ--------NKGQPCSSISY-----ENLVDPFECFMVSRD 101
                  : |:  |  :|:|   :           | |    ::     :|     :|  :
Db         63 YFETSTKDDTTPEMWLGFNDRTTEGNFQWTDGSPNDFTAWVGSNPDNYGSGEDCTQMVMG 122

Qy        102 TRLREWFKVDCEQ-QHSFICK 121
                | |  : |   :|  |||
Db        123 AGL-NWIDLPCSSTRHYLICK 142
```

RESULT 48
S28764
neurocan precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S28764
R;Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K.
J. Biol. Chem. 267, 19536-19547, 1992
A;Title: Cloning and primary structure of neurocan, a developmentally regulated, aggregat
A;Reference number: S28764; MUID:92406907; PMID:1326557
A;Accession: S28764
A;Molecule type: mRNA
A;Residues: 1-1257 <RAU>
A;Cross-references: UNIPROT:P55067; EMBL:M97161; NID:g205649; PIDN:AAC37679.1; PID:g20565
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGF
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-1257/Product: neurocan #status predicted <MAT>
F;176-253/Domain: link protein repeat homology <LNK1>
F;274-355/Domain: link protein repeat homology <LNK2>
F;364-366/Region: cell attachment (R-G-D) motif
F;953-984/Domain: EGF homology <EGF>
F;1029-1149/Domain: C-type lectin homology <LCH>
F;1156-1212/Domain: complement factor H repeat homology <FHD>
F;121,339,737,967,1164/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;372,410/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
F;944/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental

Query Match 18.7%; Score 130; DB 2; Length 1257;
Best Local Similarity 28.3%; Pred. No. 3e-05;
Matches 39; Conservative 14; Mismatches 49; Indels 36; Gaps 8;

```
Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              |  ||     :||: |     |  ||| |  :|  ||| || :  |  |:::  : |
Db       1029 CDRGWHKFQGHCYRYFAHRRAWEDAERDCRRRA--GHLTSVHSPEEHKFINSFGHENS-- 1084

Qy         64 LTRYIWIGLR----------VQNKGQPCSSISYEN----LVDPF-----EC-FMVSRDTR 103
                  ||||              | |     : |||      | |     :|  ||: :
Db       1085 -----WIGLNDRTVERDFQWTDNTG-----LQYENWREKQPDNFFAGGEDCVVMVAHEN- 1133

Qy        104 LREWFKVDCEQQHSFICK 121
                |  | |     ::||
Db       1134 -GRWNDVPCNYNLPYVCK 1150
```

RESULT 49
I83377
regenerating protein III (reg III) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I60296; I83377
R;Suzuki, Y.; Yonekura, H.; Watanabe, T.; Unno, M.; Moriizumi, S.; Miyashita, H.; Okamoto
Gene 144, 315-316, 1994
A;Title: Structure and expression of a novel rat RegIII gene.

```
A;Reference number: I60296; MUID:94314238; PMID:8039722
A;Accession: I60296
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-174 <RES>
A;Cross-references: UNIPROT:P35231; GB:D23676; NID:g471157; PIDN:BAA04904.1; PID:g471158
A;Accession: I83377
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-174 <RE2>
A;Cross-references: GB:D26078; NID:g471159; PIDN:BAA05071.1; PID:g471160
C;Genetics:
A;Gene: RegIII
A;Introns: 25/1; 64/3; 110/3; 153/1
C;Superfamily: tetranectin; C-type lectin homology
F;39-170/Domain: C-type lectin homology <LCH>

  Query Match             18.5%;  Score 128.5;  DB 2;  Length 174;
  Best Local Similarity   25.4%;  Pred. No. 4.8e-06;
  Matches   36;  Conservative   21;  Mismatches   54;  Indels   31;  Gaps    4;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              || |  :   |||        :|  |:  | ::   |||:|: :  ||||| : |   :
Db         39 CPMGSKAYRSYCYTLVTTLKSWFQADLAC-QKRPSGHLVSILSGGEASFVSS-LVTGRVN 96

Qy         64 LTRYIWIGLRVQNKGQ-----------------------PCSSISYENLVDPFECFMVSR 100
                : |||||     ||                       | |:::  |      |  ::
Db         97 NNQDIWIGLHDPTMGQQPNGGGWEWSNSDVLNYLNWDGDPSSTVNRGN------CGSLTA 150

Qy        101 DTRLREWFKVDCEQQHSFICKF 122
               :   :|    |: :  |:|||
Db        151 TSEFLKWGDHHCDVELPFVCKF 172


RESULT 50
T42710
mannose receptor, macrophage - mouse
N;Alternate names: lambda lectin; phospholipase A2 receptor
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42710
R;Wu, K.; Yuan, J.; Lasky, L.A.
J. Biol. Chem. 271, 21323-21330, 1996
A;Title: Characterization of a novel member of the macrophage mannose receptor type C le
A;Reference number: Z22235; MUID:96355501; PMID:8702911
A;Accession: T42710
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1479 <WUK>
A;Cross-references: UNIPROT:Q64449; EMBL:U56734; NID:g1336073; PID:g1336074; PIDN:AAC527
C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II re
C;Keywords: membrane protein; receptor
F;186-227/Domain: fibronectin type II repeat homology <2FR>

  Query Match             18.3%;  Score 127.5;  DB 2;  Length 1479;
  Best Local Similarity   29.1%;  Pred. No. 6.6e-05;
  Matches   44;  Conservative   16;  Mismatches   54;  Indels   37;  Gaps    8;

Qy          4 CPSGWSSTD--RYCYKPFKQE-----MTWASAERFCSEQAKGGHLLSVETALEASFVDNV 56
              || || |    |:||| |  |      :|  |   | |   |  |||: :  |  || ::
Db        668 CPQGWVSDPKLRHCYKVFSSERLQEKKSWIQALGVCRE--LGAQLLSLASYEEEHFVAHM 725

Qy         57 LYANK--------EYLTRYIWIGLRVQNKGQPCSSISY---ENLVDPFECFMVSR----- 100
              |  ||          :   : ||||   |:  |    |:   : |   :  |  ||
Db        726 L--NKIFGESEPESHEQHWFWIGL---NRRDPREGHSWRWSDGLGFSYHNFARSRHDDDD 780

Qy        101 -------DTRLREWFKVDCEQQHSFICKFTR 124
                    |    :|  : |: |  :|||  |
Db        781 IRGCAVLDLASLQWVPMQCQTQLDWICKIPR 811


Search completed: May  2, 2005, 16:02:20
Job time : 22 secs
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OM protein - protein search, using sw model

Run on: May 2, 2005, 15:59:06 ; Search time 68 Seconds
(without alignments)
948.853 Million cell updates/sec

Title: US-10-749-387-1
Perfect score: 695
Sequence: 1 DLECPSGWSSTDRYCYKPFK.....WFKVDCEQQHSFICKFTRPR 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	658	94.7	127	1	CHBA_CROHO	P81508 crotalus ho
2	371	53.4	155	2	Q9DEA2	Q9dea2 agkistrodon
3	364	52.4	155	2	Q8JIV6	Q8jiv6 agkistrodon
4	360.5	51.9	158	2	Q719L9	Q719l9 crotalus du
5	358.5	51.6	156	2	Q71RQ6	Q71rq6 trimeresuru
6	358.5	51.6	156	2	Q71RQ7	Q71rq7 trimeresuru
7	357.5	51.4	133	1	RHCA_AGKRH	P81397 agkistrodon
8	357	51.4	157	1	MMHA_AGKHA	Q9ygg9 agkistrodon
9	353.5	50.9	156	2	Q71RQ4	Q71rq4 trimeresuru
10	351.5	50.6	156	2	Q71RQ2	Q71rq2 trimeresuru
11	335	48.2	142	2	Q9PSM6	Q9psm6 bothrops ja
12	332.5	47.8	129	2	Q7LZ71	Q7lz71 trimeresuru
13	326.5	47.0	131	1	ABA1_TRIAB	P81111 trimeresuru
14	320.5	46.1	129	1	RHCB_AGKRH	P81398 agkistrodon
15	314.5	45.3	132	1	ABBA_TRIAB	P81115 trimeresuru
16	314.5	45.3	158	2	Q8AYA5	Q8aya5 agkistrodon
17	311	44.7	133	1	BOTA_BOTJA	P22029 bothrops ja
18	310.5	44.7	158	2	Q8AV97	Q8av97 trimeresuru
19	309.5	44.5	158	2	Q8UVC6	Q8uvc6 agkistrodon
20	309.5	44.5	158	2	Q71RQ1	Q71rq1 trimeresuru
21	306.5	44.1	134	1	ABA2_TRIAB	P81112 trimeresuru
22	304.5	43.8	154	2	Q8JIV9	Q8jiv9 agkistrodon
23	304.5	43.8	154	2	Q9YGN5	Q9ygn5 agkistrodon
24	302.5	43.5	146	2	Q98UJ0	Q98uj0 trimeresuru
25	302.5	43.5	152	1	IXA_TRIFL	P23806 trimeresuru
26	300.5	43.2	158	2	Q8JGT7	Q8jgt7 trimeresuru
27	300.5	43.2	158	2	Q6TPH0	Q6tph0 trimeresuru
28	293.5	42.2	158	1	CVXA_CRODU	O93426 crotalus du
29	292.5	42.1	152	2	Q9DG39	Q9dg39 agkistrodon
30	288.5	41.5	152	2	Q8JIW0	Q8jiw0 agkistrodon
31	288.5	41.5	152	2	Q9DEF9	Q9def9 agkistrodon
32	288	41.4	136	2	Q9I841	Q9i841 agkistrodon
33	287.5	41.4	152	2	Q9IAM1	Q9iam1 agkistrodon
34	275.5	39.6	152	2	Q71RR4	Q71rr4 trimeresuru
35	273.5	39.4	158	2	Q696W1	Q696w1 vipera lebe
36	268.5	38.6	121	2	Q7SZV0	Q7szv0 agkistrodon
37	265.5	38.2	131	2	Q7T248	Q7t248 echis carin
38	262	37.7	156	2	Q6T7B6	Q6t7b6 bitis gabon
39	256.5	36.9	133	1	ECHA_ECHCA	P81017 echis carin
40	255.5	36.8	146	2	Q8AYA4	Q8aya4 agkistrodon
41	252.5	36.3	123	1	ABA4_TRIAB	P81114 trimeresuru
42	251.5	36.2	152	2	Q6X5T3	Q6x5t3 bitis ariet
43	249.5	35.9	146	2	Q9IAM0	Q9iam0 agkistrodon
44	249.5	35.9	148	1	CVXB_CRODU	O93427 crotalus du
45	248.5	35.8	146	2	Q8JIW1	Q8jiw1 agkistrodon
46	246.5	35.5	148	2	Q71RP8	Q71rp8 trimeresuru
47	244	35.1	157	2	Q6T7B5	Q6t7b5 bitis gabon
48	243.5	35.0	157	2	Q7T2Q1	Q7t2q1 echis multi
49	242.5	34.9	131	2	Q7LZK5	Q7lzk5 bitis ariet
50	242.5	34.9	148	2	Q71RP9	Q71rp9 trimeresuru
51	237.5	34.2	131	2	Q9PSM9	Q9psm9 echis carin
52	225.5	32.4	146	2	Q9I840	Q9i840 agkistrodon
53	219.5	31.6	148	2	Q8AV98	Q8av98 trimeresuru
54	218.5	31.4	123	2	Q7LZ72	Q7lz72 vipera russ
55	218.5	31.4	148	2	Q719L8	Q71918 crotalus du
56	217.5	31.3	146	2	Q7T045	Q7t045 vipera lebe
57	217.5	31.3	148	2	Q6X5T2	Q6x5t2 bitis ariet
58	217	31.2	149	2	Q8UVC7	Q8uvc7 agkistrodon
59	215.5	31.0	124	2	Q90WL9	Q90wl9 agkistrodon
60	215.5	31.0	146	2	Q8JGT6	Q8jgt6 trimeresuru
61	215.5	31.0	148	2	Q6X5T0	Q6x5t0 echis ocell
62	214	30.8	149	2	Q8AYA3	Q8aya3 agkistrodon
63	212.5	30.6	148	2	Q6X5S3	Q6x5s3 echis pyram
64	212.5	30.6	148	2	Q6X5S7	Q6x5s7 echis ocell
65	212.5	30.6	148	2	Q6X5S8	Q6x5s8 echis carin

ALIGNMENTS

RESULT 1
CHBA_CROHO
ID CHBA_CROHO STANDARD; PRT; 127 AA.
AC P81508;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CHH-B alpha subunit.
OS Crotalus horridus horridus (Timber rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8747;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96420502; PubMed=8823201; DOI=10.1021/bi960704e;
RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
RA Smith A.I., Lopez J.A., Berndt M.C.;
RT "Binding of a novel 50-kilodalton alboaggregin from Trimeresurus
RT albolabris and related viper venom proteins to the platelet membrane
RT glycoprotein Ib-IX-V complex. Effect on platelet aggregation and
RT glycoprotein Ib-mediated platelet activation.";
RL Biochemistry 35:12629-12639(1996).
CC -!- FUNCTION: Binds to platelet GPiB/IX receptor system, inhibits VWF
CC binding, and stimulates agglutination.
CC -!- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSSP; P22030; 1IJK.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.

```
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Direct protein sequencing; Lectin.
FT   DOMAIN       11    121       C-type lectin.
FT   DISULFID      4     15       By similarity.
FT   DISULFID     32    120       By similarity.
FT   DISULFID     81     81       Interchain (with C-92 in beta chain)
FT                                (Potential).
FT   DISULFID     95    112       By similarity.
SQ   SEQUENCE   127 AA;  15162 MW;  B5DA100D383E3547 CRC64;

  Query Match             94.7%;  Score 658;  DB 1;  Length 127;
  Best Local Similarity   95.2%;  Pred. No. 1.1e-61;
  Matches  120;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| |||||||||||||| |||||||||| ||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGRHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||  |||||||:|||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSIYSENLVDPFDCFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 2
Q9DEA2
ID   Q9DEA2      PRELIMINARY;      PRT;   155 AA.
AC   Q9DEA2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Agkicetin alpha subunit precursor.
GN   Name=GPIbA1;
OS   Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Deinagkistrodon.
OX   NCBI_TaxID=36307;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chen Y.L., Hong T.M., Chang T., Tsai I.H.;
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF102901; AAG42040.1; -.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Signal.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        24    155       agkicetin alpha subunit.
SQ   SEQUENCE   155 AA;  17798 MW;  92B40281A797AACD CRC64;

  Query Match             53.4%;  Score 371;  DB 2;  Length 155;
  Best Local Similarity   53.4%;  Pred. No. 3.3e-31;
  Matches   71;  Conservative   20;  Mismatches   32;  Indels   10;  Gaps    3;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|  ||||  |:||:|||   ||  |||||:||| ||||:| |:| || ||  ||  | :
Db         24 DCLPGWSSYIRFCYQPFKLLKTWEDAERFCTEQANGGHLVSFESAREADFVAGVLSENIK 83

Qy         63 YLTRYIWIGLRVQNKGQPCSS-------ISYENLVDPF--ECFMVSRDTRLREWFKVDCE 113
                 :  |:||||||||:|| |||       :||||||:||  :||:: :||  | |  | |
Db         84 -IKPYVWIGLRVQNEGQQCSSKWSDSSKVSYENLVEPFSKKCFVLKKDTGFRTWENVYCG 142

Qy        114 QQHSFICKFTRPR 126
              :| |:||: :||
Db        143 LKHVFMCKYLKPR 155


RESULT 3
Q8JIV6
ID   Q8JIV6      PRELIMINARY;      PRT;   155 AA.
AC   Q8JIV6;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Antithrombin A A-chain.
OS   Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Deinagkistrodon.
OX   NCBI_TaxID=36307;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yu H., Xiang K., Wang Y., Liu J.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY091762; AAM22790.1; -.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   155 AA;  17715 MW;  66E55C95E997A1D7 CRC64;

  Query Match             52.4%;  Score 364;  DB 2;  Length 155;
  Best Local Similarity   52.6%;  Pred. No. 1.8e-30;
  Matches   70;  Conservative   20;  Mismatches   33;  Indels   10;  Gaps    3;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|  |||   |:||:|||   ||  |||||:||| ||||:| |:| || ||  ||  | :
Db         24 DCLPGWSCYIRFCYQPFKLLKTWEDAERFCTEQANGGHLVSFESAGEADFVAGVLSENIK 83

Qy         63 YLTRYIWIGLRVQNKGQPCSS-------ISYENLVDPF--ECFMVSRDTRLREWFKVDCE 113
                 :  |:||||||||:|| |||       :||||||:||  :||:: :||  | |  | |
Db         84 -IKPYVWIGLRVQNEGQQCSSKWSDSSKVSYENLVEPFSKKCFVLKKDTGFRTWENVYCG 142

Qy        114 QQHSFICKFTRPR 126
              :| |:||: :||
Db        143 LKHVFMCKYLKPR 155


RESULT 4
Q719L9
ID   Q719L9      PRELIMINARY;      PRT;   158 AA.
AC   Q719L9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Crotocetin-1.
OS   Crotalus durissus terrificus (South American rattlesnake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Crotalus.
OX   NCBI_TaxID=8732;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Radis-Baptista G., Camargo A.C.M., Yamane T.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF541883; AAQ11364.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
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```
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   158 AA;  18199 MW;  9F43B3164691D1E9 CRC64;

  Query Match           51.9%;  Score 360.5;  DB 2;  Length 158;
  Best Local Similarity   47.4%;  Pred. No. 4.4e-30;
  Matches   64;  Conservative   27;  Mismatches   35;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :||||||: |:|||:  ||  ||  || ||::|||| ||:|||:| || ||  ::  |
Db         24 DFDCPSGWSAYDQYCYRVIKQLKTWEDAEWFCTKQAKGAHLVSVESAGEADFVAQLVAEN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
                :    |:|||||:||||| |       ||::||||:  :  :|| : ::|   :|:  |
Db         84 IKQNKYYVWIGLRIQNKGQQCSTKWSDGSSVNYENLLKSYSKKCFGLKKETEFLQWYNTD 143

Qy        112 CEQQHSFICKFTRPR 126
              ||::: |:|||   |
Db        144 CEEKNLFVCKFPPQR 158


RESULT 5
Q71RQ6
ID   Q71RQ6      PRELIMINARY;      PRT;   156 AA.
AC   Q71RQ6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Stejaggregin-B alpha chain-2.
OS   Trimeresurus stejnegeri (Chinese green tree viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=39682;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Lee W.-H., Liu H., Zhang Y.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF354919; AAQ15161.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   156 AA;  17984 MW;  C08E54F9955369FDF CRC64;

  Query Match           51.6%;  Score 358.5;  DB 2;  Length 156;
  Best Local Similarity   52.2%;  Pred. No. 7e-30;
  Matches   70;  Conservative   18;  Mismatches   35;  Indels   11;  Gaps    4;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| |||  :|||:  ||  ||  ||||| :| || ||:|:|:  || ||   |  | :
Db         24 DCPSDWSSFKQYCYQIIKQLKTWEDAERFCMDQVKGAHLVSIESYREAVFVAQQLSENVK 83

Qy         63 YLTRY-IWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVDC 112
                |:| :|||| | |||| |       ||:|||||| |   :||:: : |  |:|| | |
Db         84 -TTKYDVWIGLSVVNKGQQCSSEWSDGSSVSYENLVKPLSKKCFVLKKGTEFRKWFNVAC 142

Qy        113 EQQHSFICKFTRPR 126
              ||:| |:||| |||
Db        143 EQKHLFMCKFLRPR 156


RESULT 6
Q71RQ7
ID   Q71RQ7      PRELIMINARY;      PRT;   156 AA.
AC   Q71RQ7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Stejaggregin-B alpha chain-1.
OS   Trimeresurus stejnegeri (Chinese green tree viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=39682;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Lee W.-H., Liu H., Zhang Y.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF354918; AAQ15160.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   156 AA;  17924 MW;  4AAF11F94167D58F CRC64;

  Query Match           51.6%;  Score 358.5;  DB 2;  Length 156;
  Best Local Similarity   52.2%;  Pred. No. 7e-30;
  Matches   70;  Conservative   18;  Mismatches   35;  Indels   11;  Gaps    4;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| |||  :|||:  ||  ||  ||||| :| || ||:|:|:  || ||   |  | :
Db         24 DCPSDWSSFKQYCYQIIKQLKTWEDAERFCMDQVKGAHLVSIESYREAVFVAQQLSENVK 83

Qy         63 YLTRY-IWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVDC 112
                |:| :|||| | |||| |       ||:|||||| |   :||:: : |  |:|| | |
Db         84 -TTKYDVWIGLSVVNKGQQCSSEWSDGSSVSYENLVKPLSKKCFVLKKGTEFRKWFNVAC 142

Qy        113 EQQHSFICKFTRPR 126
              ||:| |:||| |||
Db        143 EQKHLFMCKFLRPR 156


RESULT 7
RHCA_AGKRH
ID   RHCA_AGKRH     STANDARD;      PRT;   133 AA.
AC   P81397;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Rhodocetin alpha subunit.
OS   Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Calloselasma.
OX   NCBI_TaxID=8717;
RN   [1]
RP   SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY.
RC   TISSUE=Venom;
RX   MEDLINE=99303998; PubMed=10360956; DOI=10.1021/bi982132z;
RA   Wang R., Kini R.M., Chung M.C.M.;
RT   "Rhodocetin, a novel platelet aggregation inhibitor from the venom of
RT   Calloselasma rhodostoma (Malayan pit viper): synergistic and
RT   noncovalent interaction between its subunits.";
RL   Biochemistry 38:7584-7593(1999).
CC   -!- FUNCTION: A potent inhibitor of collagen-induced platelet
CC       aggregation. Individually, neither subunit inhibits platelet
CC       aggregation. Both subunits are essential.
CC   -!- SUBUNIT: Heterodimer of one alpha and one beta subunit held
CC       together by noncovalent interactions rather than by intersubunit
CC       disulfide bridges.
CC   -!- SUBCELLULAR LOCATION: Secreted.
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CC   -!- MASS SPECTROMETRY: MW=15955.90; MW_ERR=1.44; METHOD=Electrospray;
CC       RANGE=1-133; NOTE=Ref.1.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR   HSSP; P22030; 1IJK.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Direct protein sequencing; Lectin.
FT   DOMAIN        1    129       C-type lectin.
FT   DISULFID      2     13       By similarity.
FT   DISULFID     30    127       By similarity.
FT   DISULFID    102    119       By similarity.
SQ   SEQUENCE   133 AA;  15962 MW;  386EAC519DFC674D CRC64;

  Query Match             51.4%;  Score 357.5;  DB 1;  Length 133;
  Best Local Similarity   49.6%;  Pred. No. 7.5e-30;
  Matches   66;  Conservative   22;  Mismatches   36;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|| ||||| |||:|||:: || |||||:|| |  ||:|:| ||| ||| |:  | |
Db          1 DCPDGWSSTKSYCYRPFKEKKTWEEAERFCTEQEKEAHLVSMENRLEAVFVDMVMENNFE 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVDCE 113
                  ||||:::|||          ||||||| :|:  :||::   : | :|   |||
Db         61 NKIYRSWIGLKIENKGQRSNLEWSDGSSISYENLYEPYMEKCFLMDHQSGLPKWHTADCE 120

Qy        114 QQHSFICKFTRPR 126
              ::: |:|||  ||
Db        121 EKNVFMCKFQLPR 133


RESULT 8
MMHA_AGKHA
ID   MMHA_AGKHA     STANDARD;      PRT;   157 AA.
AC   Q9YGG9;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Mamushigin alpha chain precursor.
OS   Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Gloydius.
OX   NCBI_TaxID=242054;
RN   [1]
RP   SEQUENCE FROM N.A., SEQUENCE OF 22-58, SUBUNIT, AND MASS SPECTROMETRY.
RC   TISSUE=Venom;
RX   MEDLINE=98319530; PubMed=9657448;
RA   Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M.,
RA   Suzuki M., Matsui T., Titani K., Yoshioka A.;
RT   "The cDNA cloning and molecular characterization of a snake venom
RT   platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon
RT   halys blomhoffii venom.";
RL   Thromb. Haemost. 79:1199-1207(1998).
CC   -!- FUNCTION: Binds to platelet glycoprotein Ib and enhances platelet
CC       aggregation at low-shear stress. At high-shear stress, aggregation
CC       is inhibited.
CC   -!- SUBUNIT: Heterodimer of alpha and beta chains; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- MASS SPECTROMETRY: MW=16825; MW_ERR=2.7; METHOD=Electrospray;
CC       RANGE=22-157; NOTE=Ref.1.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AB019615; BAA34424.1; -.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005576; C:extracellular; IC.
DR   GO; GO:0007596; P:blood coagulation; IDA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Blood coagulation; Direct protein sequencing; Lectin; Signal.
FT   SIGNAL        1     21
FT   CHAIN        22    157       Mamushigin alpha chain.
FT   DOMAIN       34    152       C-type lectin.
FT   DISULFID     27     38       By similarity.
FT   DISULFID     55    151       By similarity.
FT   DISULFID    103    103       Interchain (with C-98 in beta chain) (By
FT                                similarity).
FT   DISULFID    126    143       By similarity.
SQ   SEQUENCE   157 AA;  18333 MW;  47DAA17891CE1865 CRC64;

  Query Match             51.4%;  Score 357;  DB 1;  Length 157;
  Best Local Similarity   50.4%;  Pred. No. 1e-29;
  Matches   68;  Conservative   24;  Mismatches   33;  Indels   10;  Gaps    3;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :||| |||  |:||| |:|:| || ||||||:||  | ||:|:|:  ||:||: ::  |
Db         24 DSDCPSDWSSNGRFCYKLFQQKMKWADAERFCTEQRTGAHLVSIESNTEAAFVNQMISEN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDP--FECFMVSRDTRLREWFKVD 111
                :  | |:|||| |||: | |       ||:|||||| |   :||::      |:|| |
Db         84 IK-KTDYVWIGLTVQNEEQQCKSRWSDRSSVSYENLVKPNSKKCFVLKEYEGSRKWFNVY 142

Qy        112 CEQQHSFICKFTRPR 126
              | |:::|:||| ||
Db        143 CGQKYAFMCKFLRPR 157


RESULT 9
Q71RQ4
ID   Q71RQ4      PRELIMINARY;      PRT;   156 AA.
AC   Q71RQ4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Stejaggregin-B alpha chain-3.
OS   Trimeresurus stejnegeri (Chinese green tree viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=39682;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Lee W.-H., Liu H., Zhang Y.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF354921; AAQ15163.1; -.
DR   EMBL; AF354922; AAQ15164.1; -.
DR   EMBL; AF354920; AAQ15162.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   156 AA;  17972 MW;  C09FB50944D76FDF CRC64;

  Query Match             50.9%;  Score 353.5;  DB 2;  Length 156;
  Best Local Similarity   51.5%;  Pred. No. 2.4e-29;
  Matches   69;  Conservative   18;  Mismatches   36;  Indels   11;  Gaps    4;
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Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| |||  :|||:  ||  ||  ||||| :| || ||:|:|:  || ||   |  | :
Db         24 DCPSDWSSFKQYCYQIIKQLKTWEDAERFCMDQVKGAHLVSIESYREAVFVAQQLSENVK 83

Qy         63 YLTRY-IWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVDC 112
                |:| :| || | |||| |       ||:|||||| |   :||:: : |  |:|| | |
Db         84 -TTKYDVWTGLSVVNKGQQCSSEWSDGSSVSYENLVKPLSKKCFVLKKGTEFRKWFNVAC 142

Qy        113 EQQHSFICKFTRPR 126
              ||:| |:||| |||
Db        143 EQKHLFMCKFLRPR 156


RESULT 10
Q71RQ2
ID   Q71RQ2      PRELIMINARY;      PRT;   156 AA.
AC   Q71RQ2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Stejaggregin-B alpha chain-4.
OS   Trimeresurus stejnegeri (Chinese green tree viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=39682;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Lee W.-H., Liu H., Zhang Y.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF354923; AAQ15165.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   156 AA;  17824 MW;  4AAF0D894167D58F CRC64;

  Query Match             50.6%;  Score 351.5;  DB 2;  Length 156;
  Best Local Similarity   51.5%;  Pred. No. 3.9e-29;
  Matches   69;  Conservative   18;  Mismatches   36;  Indels   11;  Gaps    4;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| |||  :|||:  ||  ||  ||||| :| || ||:|:|:  || ||   |  | :
Db         24 DCPSDWSSFKQYCYQIIKQLKTWEDAERFCMDQVKGAHLVSIESYREAVFVAQQLSENVK 83

Qy         63 YLTRY-IWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVDC 112
                |:| :|||| | |||| |       ||:|||||| |   :||:: : |  |:|| | |
Db         84 -TTKYDVWIGLSVVNKGQQCSSEWSDGSSVSYENLVKPLSKKCFVLKKGTEFRKWFNVAC 142

Qy        113 EQQHSFICKFTRPR 126
              ||:| |:|||  ||
Db        143 EQKHLFMCKFLGPR 156


RESULT 11
Q9PSM6
ID   Q9PSM6      PRELIMINARY;      PRT;   142 AA.
AC   Q9PSM6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Platelet glycoprotein IB-binding protein alpha subunit, GPIB-BP alpha
DE   subunit.
OS   Bothrops jararaca (Jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8724;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96209990; PubMed=8631868; DOI=10.1074/jbc.271.18.10635;
RA   Kawasaki T., Pujimura Y., Usami Y., Suzuki M., Miura S., Sakurai Y.,
RA   Makita K., Taniuchi Y., Hirano K., Titani K.;
RT   "Complete amino acid sequence and identification of the platelet
RT   glycoprotein Ib-binding site of jararaca GPIb-BP, a snake venom
RT   protein isolated from Bothrops jararaca.";
RL   J. Biol. Chem. 271:10635-10639(1996).
DR   HSSP; P22029; 1FVU.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   142 AA;  16720 MW;  E28EFDEBEF922004 CRC64;

  Query Match             48.2%;  Score 335;  DB 2;  Length 142;
  Best Local Similarity   47.1%;  Pred. No. 1.9e-27;
  Matches   65;  Conservative   23;  Mismatches   36;  Indels   14;  Gaps    3;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTW-----ASAERFCSEQAKGGHLLSVETALEASFVDNVL 57
              |||| ||:  :|||| |:|: :|       |||||||||||||:|:|:  || ||  ::
Db          5 ECPSDWSTHRQYCYKFFQQKESWDDRSEYDAERFCSEQAKGGHLVSIESDEEADFVAQLV 64

Qy         58 YANKEYLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWF 108
                |      |:|||||::|| | |       ||:||||||  :  :|| : :    |:|
Db         65 APNIGKSKYYVWIGLRIENKKQQCSSKWSDYSSVSYENLVRGNVKKCFALEKKQGFRKWV 124

Qy        109 KVDCEQQHSFICKFTRPR 126
              :|| : : |:||| |||
Db        125 NIDCVEGNPFVCKFIRPR 142


RESULT 12
Q7LZ71
ID   Q7LZ71      PRELIMINARY;      PRT;   129 AA.
AC   Q7LZ71;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Coagulation factor IX-binding protein A chain.
OS   Trimeresurus flavoviridis (Habu) (Protobothrops flavoviridis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=88087;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96318509; PubMed=8749314;
RA   Atoda H., Ishikawa M., Yoshihara E., Sekiya F., Morita T.;
RT   "Blood coagulation factor IX-binding protein from the venom of
RT   Trimeresurus flavoviridis: purification and characterization.";
RL   J. Biochem. 118:965-973(1995).
DR   PIR; JC4329; JC4329.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   129 AA;  14640 MW;  225F3C7D841D8C76 CRC64;

  Query Match             47.8%;  Score 332.5;  DB 2;  Length 129;
  Best Local Similarity   47.7%;  Pred. No. 3.2e-27;
  Matches   61;  Conservative   23;  Mismatches   35;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||||||| : :||||||   ||  |||||:||||||||:|:|:| || ||  ::  | :
Db          1 DCPSGWSSYEGHCYKPFKLYKTWDDAERFCTEQAKGGHLVSIESAGEADFVAQLVTENIQ 60
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Qy          63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVDCE 113
                  |:|||||| | : |       ||:|||| ::     |  : ::|  |:|  : |
Db          61 NTKSYVWIGLRVQGKEKQCSSEWSDGSSVSYENWIEAESKTCLGLEKETGFRKWVNIYCG 120

Qy         114 QQHSFICK 121
               ||: |:|:
Db         121 QQNPFVCE 128


RESULT 13
ABA1_TRIAB
ID   ABA1_TRIAB     STANDARD;      PRT;   131 AA.
AC   P81111;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Alboaggregin A subunit 1.
OS   Trimeresurus albolabris (White-lipped pit viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=8765;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=98189535; PubMed=9531050;
RA   Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA   Calvete J.J., Niewiarowski S.;
RT   "Alboaggregins A and B. Structure and interaction with human
RT   platelets.";
RL   Thromb. Haemost. 79:609-613(1998).
CC   -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC       agglutination.
CC   -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4, disulfide-
CC       linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR   HSSP; P23806; 1J34.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Direct protein sequencing; Lectin.
FT   DOMAIN        1    131       C-type lectin.
FT   DISULFID      2     13       By similarity.
FT   DISULFID     30    127       By similarity.
FT   DISULFID    102    119       By similarity.
SQ   SEQUENCE   131 AA;  15427 MW;  B3569F5BF91F6624 CRC64;

  Query Match            47.0%;  Score 326.5;  DB 1;  Length 131;
  Best Local Similarity  46.6%;  Pred. No. 1.4e-26;
  Matches   61;  Conservative   20;  Mismatches   41;  Indels    9;  Gaps    2;

Qy           3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
               :||| ||| |:|||: ||:  ||  |||||||||  |||:|:|:| || ||  ::  |
Db           1 DCPSDWSSYDQYCYRVFKRIQTWEDAERFCSEQANDGHLVSIESAGEADFVTQLVSENIR 60

Qy          63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVD--PFECFMVSRDTRLREWFKVDCE 113
                  |:|||||| ||| |       ||: |:|| :    :|: : :    | |  | |
Db          61 SEKHYVWIGLRVQGKGQQCSSEWSDGSSVHYDNLQENKTRKCYGLEKRAEFRTWSNVYCG 120

Qy         114 QQHSFICKFTR 124
                :: |:||| |
Db         121 HEYPFVCKFXR 131


RESULT 14
RHCB_AGKRH
ID   RHCB_AGKRH     STANDARD;      PRT;   129 AA.
AC   P81398;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Rhodocetin beta subunit.
OS   Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Calloselasma.
OX   NCBI_TaxID=8717;
RN   [1]
RP   SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY.
RC   TISSUE=Venom;
RX   MEDLINE=99303998; PubMed=10360956; DOI=10.1021/bi982132z;
RA   Wang R., Kini R.M., Chung M.C.M.;
RT   "Rhodocetin, a novel platelet aggregation inhibitor from the venom of
RT   Calloselasma rhodostoma (Malayan pit viper): synergistic and
RT   noncovalent interaction between its subunits.";
RL   Biochemistry 38:7584-7593(1999).
CC   -!- FUNCTION: A potent inhibitor of collagen-induced platelet
CC       aggregation. Individually, neither subunit inhibits platelet
CC       aggregation. Both subunits are essential.
CC   -!- SUBUNIT: Heterodimer of one alpha and one beta subunit held
CC       together by noncovalent interactions rather than by intersubunit
CC       disulfide bridges.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- MASS SPECTROMETRY: MW=15184.53; MW_ERR=2.74; METHOD=Electrospray;
CC       RANGE=1-129; NOTE=Ref.1.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR   HSSP; P22030; 1IJK.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Direct protein sequencing; Lectin.
FT   DOMAIN        3    125       C-type lectin.
FT   DISULFID      4     15       By similarity.
FT   DISULFID     98    115       By similarity.
SQ   SEQUENCE   129 AA;  15190 MW;  EF4B318FAAC807AE CRC64;

  Query Match            46.1%;  Score 320.5;  DB 1;  Length 129;
  Best Local Similarity  44.5%;  Pred. No. 6e-26;
  Matches   57;  Conservative   29;  Mismatches   39;  Indels    3;  Gaps    2;

Qy           1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
               |  ||: ||::  |||||||:: ||  |||||::||: |||:|: :| || |:|  |:  |
Db           1 DFRCPTTWSASKLYCYKPFKEKKTWIEAERFCAKQAENGHLVSIGSAAEADFLDLVIVVN 60

Qy          61 KEYLTRYIWIGLRVQN-KGQPCSSISYENLVDPF--ECFMVSRDTRLREWFKVDCEQQHS 117
                :     | ||  :| |    :|:||||| :|:  :||:|       :|:| |||:::
Db          61 FDKQRYRAWTGLTERNLKWTNGASVSYENLYEPYIRKCFVVQPWEGKSKWYKADCEEKNA 120

Qy         118 FICKFTRP 125
               |:||| :|
Db         121 FLCKFPKP 128


RESULT 15
ABBA_TRIAB
ID   ABBA_TRIAB     STANDARD;      PRT;   132 AA.
AC   P81115;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Alboaggregin B alpha subunit.
OS   Trimeresurus albolabris (White-lipped pit viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=8765;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=98189535; PubMed=9531050;
RA   Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
```

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RA   Calvete J.J., Niewiarowski S.;
RT   "Alboaggregins A and B. Structure and interaction with human
RT   platelets.";
RL   Thromb. Haemost. 79:609-613(1998).
CC   -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC       agglutination.
CC   -!- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR   HSSP; P23806; 1J34.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Direct protein sequencing; Lectin.
FT   DOMAIN        1    132       C-type lectin.
FT   DISULFID      2     13       By similarity.
FT   DISULFID     30    127       By similarity.
FT   DISULFID     79     79       Interchain (with C-75 in beta chain) (By
FT                                similarity).
FT   DISULFID    102    119       By similarity.
SQ   SEQUENCE   132 AA;  15419 MW;  6FAE64820383F16F CRC64;

  Query Match             45.3%;  Score 314.5;  DB 1;  Length 132;
  Best Local Similarity   46.5%;  Pred. No. 2.7e-25;
  Matches   60;  Conservative   20;  Mismatches   40;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| |||  :|||:  |:  ||  || ||||||  |||:|:|:  || ||  :|  |
Db          1 DCPSDWSSFKQYCYQIVKELKTWEDAEXFCSEQANDGHLVSIESYREAVFVAELLSENVX 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                : |||| |||| | |        ||::||||:     :||:: :::  | |  | ||
Db         61 XXKYHXWIGLSVQNKXQQCSSEWSDGSSVTYENLIXXXXXKCFVLKKESEFRTWSNVYCE 120

Qy        114 QQHSFICKF 122
              |:| |:|||
Db        121 QKHIFMCKF 129


RESULT 16
Q8AYA5
ID   Q8AYA5     PRELIMINARY;      PRT;   158 AA.
AC   Q8AYA5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Agglucetin-alpha 2 subunit precursor.
OS   Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Deinagkistrodon.
OX   NCBI_TaxID=36307;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21542539; PubMed=11686327;
RA   Wang W.J., Huang T.F.;
RT   "A novel tetrameric venom protein, agglucetin from Agkistrodon acutus,
RT   acts as a glycoprotein Ib agonist.";
RL   Thromb. Haemost. 86:1077-1086(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22839357; PubMed=12958616;
RA   Wang W.-J., Ling Q.-D., Liau M.-Y., Huang T.-F.;
RT   "A tetrameric glycoprotein Ib-binding protein, agglucetin, from
RT   Formosan pit viper: structure and interaction with human platelets.";
RL   Thromb. Haemost. 90:465-475(2003).
DR   EMBL; AF540646; AAN23125.1; -.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Signal.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        24    158       agglucetin-alpha 2 subunit.
SQ   SEQUENCE   158 AA;  17977 MW;  9D0A9C936ABEA5E4 CRC64;

  Query Match             45.3%;  Score 314.5;  DB 2;  Length 158;
  Best Local Similarity   43.5%;  Pred. No. 3.2e-25;
  Matches   57;  Conservative   25;  Mismatches   40;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  || |||: |:|||:  |:   |  |||||:||| ||||:|:|:  |  ||  ::  |
Db         24 DFNCPPGWSAYDQYCYQVIKEPKNWDDAERFCTEQADGGHLVSIESKGERDFVAQLVSQN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
                | :  ::| |||||| : |       ||:|||||:: :  :|  : |:|   :|  :
Db         84 IESVEDHVWTGLRVQNKEKQCSTEWSDGSSVSYENLLELYMRKCGALERETGFHKWINLG 143

Qy        112 CEQQHSFICKF 122
              | | : |:|||
Db        144 CIQLNPFVCKF 154


RESULT 17
BOTA_BOTJA
ID   BOTA_BOTJA     STANDARD;      PRT;   133 AA.
AC   P22029;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Botrocetin, alpha chain (Platelet coagglutinin).
OS   Bothrops jararaca (Jararaca).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Bothrops.
OX   NCBI_TaxID=8724;
RN   [1]
RP   SEQUENCE, AND DISULFIDE BONDS.
RC   TISSUE=Venom;
RX   MEDLINE=93157385; PubMed=8430107;
RA   Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
RA   Titani K.;
RT   "Primary structure of two-chain botrocetin, a von Willebrand factor
RT   modulator purified from the venom of Bothrops jararaca.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
RN   [2]
RP   SEQUENCE OF 1-40.
RC   TISSUE=Venom;
RX   MEDLINE=91129280; PubMed=1993206;
RA   Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
RA   Fukui H., Sugimoto M., Ruggeri Z.M.;
RT   "Isolation and chemical characterization of two structurally and
RT   functionally distinct forms of botrocetin, the platelet coagglutinin
RT   isolated from the venom of Bothrops jararaca.";
RL   Biochemistry 30:1957-1964(1991).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX   MEDLINE=22118144; PubMed=12121649; DOI=10.1016/S0969-2126(02)00787-6;
RA   Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
RA   Liddington R.C.;
RT   "Structural basis of von Willebrand factor activation by the snake
RT   toxin botrocetin.";
RL   Structure 10:943-950(2002).
CC   -!- FUNCTION: Two-chain botrocetin forms an activated complex with
CC       vWF, and the complex then binds to platelet GPIb, resulting in
CC       platelet agglutination.
CC   -!- FUNCTION: There are two distinct forms of the von Willebrand
CC       factor-dependent platelet coagglutinin. The dimeric form is 34-
CC       times more active than the one-chain botrocetin in promoting vWF
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CC       binding to platelets.
CC   -!- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.
CC       Botrocetin and vWF form a soluble complex.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR   PIR; A47267; A47267.
DR   PDB; 1FVU; X-ray; A/C=1-133.
DR   PDB; 1IJK; X-ray; B=1-133.
DR   InterPro; IPR002353; AntifreezeII.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR00356; ANTIFREEZEII.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   3D-structure; Direct protein sequencing; Lectin.
FT   DISULFID     2    13
FT   DISULFID    30   128
FT   DISULFID    80    80       Interchain (with C-75 in beta chain).
FT   DISULFID   103   120
FT   TURN         4     5
FT   STRAND       7     9
FT   TURN        10    11
FT   STRAND      12    21
FT   HELIX       23    33
FT   TURN        35    36
FT   STRAND      38    39
FT   TURN        44    45
FT   TURN        47    47
FT   HELIX       48    57
FT   TURN        58    59
FT   TURN        62    63
FT   STRAND      66    73
FT   STRAND      83    83
FT   TURN        85    86
FT   STRAND      89    89
FT   STRAND      95    95
FT   HELIX       97    99
FT   STRAND     103   107
FT   TURN       108   111
FT   STRAND     115   118
FT   TURN       120   121
FT   STRAND     124   130
SQ   SEQUENCE   133 AA;  15215 MW;  E4CF4502946AC74B CRC64;

  Query Match             44.7%;  Score 311;  DB 1;  Length 133;
  Best Local Similarity   45.9%;  Pred. No. 6.3e-25;
  Matches   61;  Conservative   24;  Mismatches   38;  Indels   10;  Gaps    3;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVET-ALEASFVDNVLYANK 61
              :||||||| :  ||| |:|:| || |||||||||||||||:|::  : |  || :::  |
Db          1 DCPSGWSSYEGNCYKFFQQKMNWADAERFCSEQAKGGHLVSIKIYSKEKDFVGDLVTKNI 60

Qy         62 EYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVDC 112
              :    | ||||||:|| : |        ||:||||:|:    :|| : :|     |  : |
Db         61 QSSDLYAWIGLRVENKEKQCSSEWSDGSSVSYENVVERTVKKCFALEKDLGFVLWINLYC 120

Qy        113 EQQHSFICKFTRP 125
                |:: |:||   |
Db        121 AQKNPFVCKSPPP 133


RESULT 18
Q8AV97
ID   Q8AV97      PRELIMINARY;      PRT;   158 AA.
AC   Q8AV97;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Flavocetin-A alpha chain.
OS   Trimeresurus flavoviridis (Habu) (Protobothrops flavoviridis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=88087;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom glands;
RX   MEDLINE=20402624; PubMed=10942790; DOI=10.1016/S0049-3848(00)00234-6;
RA   Shin Y., Okuyama I., Hasegawa J., Morita T.;
RT   "Molecular cloning of glycoprotein Ib-binding protein, flavocetin-A,
RT   which inhibits platelet aggregation.";
RL   Thromb. Res. 99:239-247(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom glands;
RA   Shin Y., Okuyama I., Hasegawa J., Morita T.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY149341; AAN72438.1; -.
DR   PDB; 1C3A; X-ray; A=24-157.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   158 AA;  18073 MW;  8C138650665CA454 CRC64;

  Query Match             44.7%;  Score 310.5;  DB 2;  Length 158;
  Best Local Similarity   42.4%;  Pred. No. 8.6e-25;
  Matches   56;  Conservative   24;  Mismatches   43;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :|  |||: |||||: | :   |  || || |  |  ||:|:|:: |  ||  ::
Db         24 DFDCIPGWSAYDRYCYQAFSKPKNWEDAESFCEEGVKTSHLVSIESSGEGDFVAQLVAEK 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
                :   :|:|||||:||| | |       ||::|||||  |  :|: : : | || || |
Db         84 IKTSFQYVWIGLRIQNKEQQCRSEWSDASSVNYENLVKQFSKKCYALKKGTELRTWFNVY 143

Qy        112 CEQQHSFICKFT 123
                |  :: |:||:|
Db        144 CGTENPFVCKYT 155


RESULT 19
Q8UVC6
ID   Q8UVC6      PRELIMINARY;      PRT;   158 AA.
AC   Q8UVC6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Antithrombin 1 A chain.
OS   Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Deinagkistrodon.
OX   NCBI_TaxID=36307;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yu H., Xiang K., Liu J.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF463522; AAL66391.1; -.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   158 AA;  17950 MW;  A73A9C895997BFD7 CRC64;

  Query Match             44.5%;  Score 309.5;  DB 2;  Length 158;
  Best Local Similarity   42.7%;  Pred. No. 1.1e-24;
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  Matches   56;  Conservative   26;  Mismatches   40;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  || |||: |:|||:  |:   |  |||||:||| ||||:|:|:  |  ||  ::  :
Db         24 DFNCPPGWSAYDQYCYQVIKEPKNWDDAERFCTEQADGGHLVSIESKGERDFVAQLVSQS 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
               | :  ::| ||||||| : |       ||:|||||:: :  :|  : |:|   :|  :
Db         84 IESVEDHVWTGLRVQNKEKQCSTEWSDGSSVSYENLLELYMRKCGALERETGFHKWINLG 143

Qy        112 CEQQHSFICKF 122
              | | : |:|||
Db        144 CIQLNPFVCKF 154


RESULT 20
Q71RQ1
ID   Q71RQ1      PRELIMINARY;      PRT;   158 AA.
AC   Q71RQ1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Stejaggregin-A alpha chain.
OS   Trimeresurus stejnegeri (Chinese green tree viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=39682;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Lee W.-H., Liu H., Zhang Y.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF354924; AAQ15166.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   158 AA;  18055 MW;  543E35789EDCC0DC CRC64;

  Query Match             44.5%;  Score 309.5;  DB 2;  Length 158;
  Best Local Similarity   45.8%;  Pred. No. 1.1e-24;
  Matches   60;  Conservative   21;  Mismatches   41;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :||||||: | |||||| :  ||  |||||:||||||||:|:|:: || ||  ::  |
Db         24 DFDCPSGWSAYDWYCYKPFNEPQTWDDAERFCTEQAKGGHLVSIESSGEADFVGQLVSEN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPCS-------SISYE--NLVDPFECFMVSRDTRLREWFKVD 111
               :    |:||||| : | | ||        || |   |  :   |  :|: |   :|  |
Db         84 IQRPEIYVWIGLRDRRKEQQCSSEWSDGTSIIYVNWNKGESQMCQGLSKWTNFLKWDNTD 143

Qy        112 CEQQHSFICKF 122
              |: :: |:|||
Db        144 CQAKNPFVCKF 154


RESULT 21
ABA2_TRIAB
ID   ABA2_TRIAB     STANDARD;      PRT;   134 AA.
AC   P81112;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Alboaggregin A subunit 2.
OS   Trimeresurus albolabris (White-lipped pit viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=8765;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=98189535; PubMed=9531050;
RA   Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA   Calvete J.J., Niewiarowski S.;
RT   "Alboaggregins A and B. Structure and interaction with human
RT   platelets.";
RL   Thromb. Haemost. 79:609-613(1998).
CC   -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC       agglutination.
CC   -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4, disulfide-
CC       linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR   HSSP; P23806; 1J34.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Direct protein sequencing; Lectin.
FT   DOMAIN        1    134       C-type lectin.
FT   DISULFID      4     15       By similarity.
FT   DISULFID     32    129       By similarity.
FT   DISULFID    104    121       By similarity.
SQ   SEQUENCE   134 AA;  15556 MW;  5F9D71FC86DE2435 CRC64;

  Query Match             44.1%;  Score 306.5;  DB 1;  Length 134;
  Best Local Similarity   42.0%;  Pred. No. 1.9e-24;
  Matches   55;  Conservative   26;  Mismatches   41;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  |  |||: |:|||: | :   |  |||||::||  |||:|:||  || ||  ::  |
Db          1 DFHCLPGWSAYDQYCYRVFNEPKNWEDAERFCAKQADSGHLVSIETMGEADFVAQLISEN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
               :    |:||||:|||| | |       ||::||||:  :  :|  : :::  |:|  :
Db         61 IQSEKHYVWIGLKVQNKEQQCSSEWSDGSSVTYENLIKLYMRKCGALEQESGFRKWINLG 120

Qy        112 CEQQHSFICKF 122
              | | : |:|||
Db        121 CIQLNPFVCKF 131


RESULT 22
Q8JIV9
ID   Q8JIV9      PRELIMINARY;      PRT;   154 AA.
AC   Q8JIV9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   C-type lectin (Agglucetin-alpha 1 subunit precursor).
OS   Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Deinagkistrodon.
OX   NCBI_TaxID=36307;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yu H., Xiang K., Wang Y., Liu J.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21542539; PubMed=11686327;
RA   Wang W.J., Huang T.F.;
RT   "A novel tetrameric venom protein, agglucetin from Agkistrodon acutus,
RT   acts as a glycoprotein Ib agonist.";
RL   Thromb. Haemost. 86:1077-1086(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
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RX   MEDLINE=22839357; PubMed=12958616;
RA   Wang W.-J., Ling Q.-D., Liau M.-Y., Huang T.-F.;
RT   "A tetrameric glycoprotein Ib-binding protein, agglucetin, from
RT   Formosan pit viper: structure and interaction with human platelets.";
RL   Thromb. Haemost. 90:465-475(2003).
DR   EMBL; AY091759; AAM22787.1; -.
DR   EMBL; AF540645; AAN23124.1; -.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Lectin; Signal.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        24    154       agglucetin-alpha 1 subunit.
SQ   SEQUENCE   154 AA;  17317 MW;  AA08E518501BECC7 CRC64;

  Query Match             43.8%;  Score 304.5;  DB 2;  Length 154;
  Best Local Similarity   41.5%;  Pred. No. 3.6e-24;
  Matches   54;  Conservative   32;  Mismatches   33;  Indels   11;  Gaps    3;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |::|  |||: |: ||: ||   ||  ||:||:|: |||||:|:|:| |  ||  ::  |
Db         24 DVDCLPGWSAYDQSCYRVFKLLKTWDDAEKFCTERPKGGHLVSIESAGERDFVAQLVSEN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVD--PFECFMVSRDTRLREWFKVD 111
              |:  |  :|:||::|:||| |       ||:|||| :    :||:: ::|  | |  ::
Db         84 KQ--TDNVWLGLKIQSKGQQCSTEWTDGSSVSYENFSEYQSKKCFVLEKNTGFRTWLNLN 141

Qy        112 CEQQHSFICK 121
              |  :::|:||
Db        142 CGSEYAFVCK 151


RESULT 23
Q9YGN5
ID   Q9YGN5      PRELIMINARY;      PRT;   154 AA.
AC   Q9YGN5;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fibrinogen clotting inhibitor A chain.
OS   Agkistrodon halys brevicaudus (Korean slamosa snake) (Gloydius halys
OS   brevicaudus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Gloydius.
OX   NCBI_TaxID=259325;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kim D.S., Koh Y.S.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF125309; AAD18055.1; -.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   154 AA;  17293 MW;  8D06F7DDFA0D140D CRC64;

  Query Match             43.8%;  Score 304.5;  DB 2;  Length 154;
  Best Local Similarity   44.6%;  Pred. No. 3.6e-24;
  Matches   58;  Conservative   20;  Mismatches   43;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  ||||| | : :||: | | |||  |||||| |||||||:|:||  || || :|:
Db         24 DFFCPSGWGSNNGHCYQAFNQRMTWEDAERFCSAQAKGGHLVSIETRAEADFVAHVVAER 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVD 111
              |    ::||||| : | | |       ||:|||| ::     |  :  |:   :|  |
Db         84 IETSPPHVWIGLRDEGKEQQCSSEWSDGSSVSYENWIEAESKTCLGLELDSNYHKWVNVY 143

Qy        112 CEQQHSFICK 121
              | |:: |:|: .
Db        144 CGQRNPFVCE 153


RESULT 24
Q98UJ0
ID   Q98UJ0      PRELIMINARY;      PRT;   146 AA.
AC   Q98UJ0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Factor XI/factor X binding protein A chain.
GN   Name=XI/Xbp-a;
OS   Trimeresurus flavoviridis (Habu) (Protobothrops flavoviridis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=88087;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venome gland;
RA   Tani A., Ogawa T., Nose T., Nikandorov N.N., Deshimaru M., Chijiwa T.,
RA   Chang C., Fukumaki Y., Ohno M.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB046491; BAB21452.1; -.
DR   HSSP; P23806; 1IXX.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   146 AA;  16461 MW;  6ADF0E032544316C CRC64;

  Query Match             43.5%;  Score 302.5;  DB 2;  Length 146;
  Best Local Similarity   44.5%;  Pred. No. 5.5e-24;
  Matches   57;  Conservative   25;  Mismatches   37;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :| ||||| : :||| |::  ||  ||| |:|||||:||:|:|:: || ||  ::  | :
Db         18 DCLSGWSSYEGHCYKAFEKYKTWEDAERVCTEQAKGAHLVSIESSGEADFVAQLVTQNMK 77

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVDCE 113
              |  |||||||||| | : |       ||:|||| ::     |  : ::|  |:|  : |
Db         78 RLDFYIWIGLRVQGKVKQCNSEWSDGSSVSYENWIEAESKTCLGLEKETDFRKWVNIYCG 137

Qy        114 QQHSFICK 121
              ||: |:|:
Db        138 QQNPFVCE 145


RESULT 25
IXA_TRIFL
ID   IXA_TRIFL      STANDARD;      PRT;   152 AA.
AC   P23806; Q91246;
DT   01-NOV-1991 (Rel. 20, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Coagulation factor IX/factor X-binding protein A chain precursor
DE   (IX/X-BP).
OS   Trimeresurus flavoviridis (Habu) (Protobothrops flavoviridis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
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OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=88087;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96184662; PubMed=8645314; DOI=10.1006/bbrc.1996.0414;
RA   Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
RT   "cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
RT   protein from snake venom.";
RL   Biochem. Biophys. Res. Commun. 220:382-387(1996).
RN   [2]
RP   SEQUENCE OF 24-152.
RC   TISSUE=Venom;
RX   MEDLINE=91332000; PubMed=1831197;
RA   Atoda H., Hyuga M., Morita T.;
RT   "The primary structure of coagulation factor IX/factor X-binding
RT   protein isolated from the venom of Trimeresurus flavoviridis. Homology
RT   with asialoglycoprotein receptors, proteoglycan core protein,
RT   tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin
RT   E.";
RL   J. Biol. Chem. 266:14903-14911(1991).
RN   [3]
RP   CHARACTERIZATION.
RC   TISSUE=Venom;
RX   PubMed=8749314;
RA   Atoda H., Ishikawa M., Yoshihara E., Sekiya F., Morita T.;
RT   "Blood coagulation factor IX-binding protein from the venom of
RT   Trimeresurus flavoviridis: purification and characterization.";
RL   J. Biochem. 118:965-973(1995).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX   MEDLINE=97331317; PubMed=9187649;
RA   Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
RT   "Structure of coagulation factors IX/X-binding protein, a heterodimer
RT   of C-type lectin domains.";
RL   Nat. Struct. Biol. 4:438-441(1997).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
RX   PubMed=10339409; DOI=10.1006/jmbi.1999.2756;
RA   Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
RT   "Crystal structure of coagulation factor IX-binding protein from habu
RT   snake venom at 2.6 A: implication of central loop swapping based on
RT   deletion in the linker region.";
RL   J. Mol. Biol. 289:103-112(1999).
CC   -!- FUNCTION: Anticoagulant protein which binds with factor IX and
CC       factor X in the presence of calcium with a 1 to 1 stoichiometry.
CC   -!- SUBUNIT: Heterodimer of chains A and B; disulfide-linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- MISCELLANEOUS: Calcium is required for ligand binding.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D83331; BAA11887.1; -.
DR   PIR; JC4690; JC4690.
DR   PDB; 1IXX; X-ray; A/C/E=24-152.
DR   PDB; 1J34; X-ray; A=24-152.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   3D-structure; Calcium; Direct protein sequencing; Lectin; Signal.
FT   SIGNAL       1     23
FT   CHAIN       24    152       Coagulation factor IX/factor X-binding
FT                               protein A chain.
FT   DOMAIN      24    152       C-type lectin.
FT   DISULFID    25     36
FT   DISULFID    53    150
FT   DISULFID   102    102       Interchain (with C-98 in chain B).
FT   DISULFID   125    142
FT   TURN        27     28
FT   STRAND      30     32
FT   TURN        33     34
FT   STRAND      35     44
FT   HELIX       46     54
FT   TURN        55     56
FT   TURN        58     59
FT   STRAND      61     62
FT   HELIX       68     81
FT   STRAND      89     95
FT   STRAND     105    105
FT   TURN       107    108
FT   STRAND     111    111
FT   STRAND     117    117
FT   HELIX      119    121
FT   STRAND     125    128
FT   HELIX      130    132
FT   TURN       133    134
FT   STRAND     137    140
FT   TURN       142    143
FT   STRAND     146    152
SQ   SEQUENCE   152 AA;  17213 MW;  FB3DDD2369009263 CRC64;

  Query Match             43.5%;  Score 302.5;  DB 1;  Length 152;
  Best Local Similarity   44.5%;  Pred. No. 5.8e-24;
  Matches   57;  Conservative   25;  Mismatches   37;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :| ||||| : :||| |::  ||  ||| |:||||| ||:|:|:: || ||  ::  | :
Db         24 DCLSGWSSYEGHCYKAFEKYKTWEDAERVCTEQAKGAHLVSIESSGEADFVAQLVTQNMK 83

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVDCE 113
               |  |||||||| | : |       ||:|||| ::     |  : ::|  |:|  : |
Db         84 RLDFYIWIGLRVQGKVKQCNSEWSDGSSVSYENWIEAESKTCLGLEKETDFRKWVNIYCG 143

Qy        114 QQHSFICK 121
              ||: |:|:
Db        144 QQNPFVCE 151


RESULT 26
Q8JGT7
ID   Q8JGT7      PRELIMINARY;      PRT;   158 AA.
AC   Q8JGT7;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   C-type lectin-like protein TMVA A chain.
OS   Trimeresurus mucrosquamatus (Taiwan habu) (Protobothrops
OS   mucrosquamatus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Protobothrops.
OX   NCBI_TaxID=103944;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22210230; PubMed=12220719; DOI=10.1016/S0041-0101(02)00144-7;
RA   Wei Q., Lu Q.M., Jin Y., Li R., Wei J.F., Wang W.Y., Xiong Y.L.;
RT   "Purification and cloning of a novel C-type lectin-like protein with
RT   platelet aggregation activity from Trimeresurus mucrosquamatus
RT   venom.";
RL   Toxicon 40:1331-1338(2002).
DR   EMBL; AY099321; AAM43808.1; -.
DR   PDB; 1V4L; X-ray; A/C/E=24-158.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
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DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Lectin.
SQ   SEQUENCE   158 AA;  18101 MW;  CD0B71F02289AA6E CRC64;

  Query Match             43.2%;  Score 300.5;  DB 2;  Length 158;
  Best Local Similarity   40.9%;  Pred. No. 9.9e-24;
  Matches   54;  Conservative   25;  Mismatches   44;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :|  |||: |||||: | :   |  || || |  |  ||:|:|:: |  ||  ::
Db         24 DFDCIPGWSAYDRYCYQAFSEPKNWEDAESFCEEGVKTSHLVSIESSGEGDFVAQLVAEK 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVD 111
               :   :|:|||||:||| | |       ||::||||      :|: : : | || || |
Db         84 IKTSFQYVWIGLRIQNKEQQCRSEWSDASSVNYENLFKQSSKKCYALKKGTELRTWFNVY 143

Qy        112 CEQQHSFICKFT 123
              | ::: |:||:|
Db        144 CGRENPFVCKYT 155


RESULT 27
Q6TPH0
ID   Q6TPH0      PRELIMINARY;      PRT;   158 AA.
AC   Q6TPH0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Mucrocetin alpha chain.
OS   Trimeresurus mucrosquamatus (Taiwan habu) (Protobothrops
OS   mucrosquamatus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Protobothrops.
OX   NCBI_TaxID=103944;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Hung C.-C., Huang K.-F., Chiou S.-H.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY390533; AAQ93686.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   158 AA;  18129 MW;  419ABE2F0344B9CA CRC64;

  Query Match             43.2%;  Score 300.5;  DB 2;  Length 158;
  Best Local Similarity   40.9%;  Pred. No. 9.9e-24;
  Matches   54;  Conservative   25;  Mismatches   44;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :|  |||: |||||: | :   |  || || |  |  ||:|:|:: |  ||  ::
Db         24 DFDCIPGWSAYDRYCYQAFSEPKNWEDAESFCEEGVKTSHLVSIESSGEGDFVAQLVAEK 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVD 111
               :   :|:|||||:||| | |       ||::||||      :|: : : | || || |
Db         84 IKTSFQYVWIGLRIQNKEQQCRSEWSDASSVNYENLFKQSSKKCYALKKGTELRTWFNVY 143

Qy        112 CEQQHSFICKFT 123
              | ::: |:||:|
Db        144 CGRENPFVCKYT 155


RESULT 28
CVXA_CRODU
ID   CVXA_CRODU     STANDARD;      PRT;   158 AA.
AC   O93426;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Convulxin alpha precursor (CVX alpha).
OS   Crotalus durissus terrificus (South American rattlesnake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Crotalus.
OX   NCBI_TaxID=8732;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 24-48; 61-68; 108-120; 139-145 AND
RP   149-153.
RC   TISSUE=Venom gland;
RX   MEDLINE=98324901; PubMed=9657980;
RA   Leduc M., Bon C.;
RT   "Cloning of subunits of convulxin, a collagen-like platelet-
RT   aggregating protein from Crotalus durissus terrificus venom.";
RL   Biochem. J. 333:389-393(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Radis-Baptista G., Camargo A.C.M., Yamane T.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 24-158.
RX   PubMed=14521935; DOI=10.1016/j.bbrc.2003.09.032;
RA   Murakami M.T., Zela S.P., Gava L.M., Michelan-Duarte S.,
RA   Cintra A.C.O., Arni R.K.;
RT   "Crystal structure of the platelet activator convulxin, a disulfide-
RT   linked alpha4beta4 cyclic tetramer from the venom of Crotalus durissus
RT   terrificus.";
RL   Biochem. Biophys. Res. Commun. 310:478-482(2003).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 26-158.
RX   PubMed=14684891;
RA   Batuwangala T., Leduc M., Gibbins J.M., Bon C., Jones E.Y.;
RT   "Structure of the snake-venom toxin convulxin.";
RL   Acta Crystallogr. D 60:46-53(2004).
CC   -!- FUNCTION: Binds to the platelet and collagen receptor,
CC       glycoprotein VI (GPVI).
CC   -!- SUBUNIT: Heterooctamer of four alpha chains and four beta chains;
CC       disulfide-linked.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y16348; CAA76181.1; -.
DR   EMBL; AF541882; AAQ11363.1; -.
DR   PDB; 1UMR; X-ray; A/B=24-157.
DR   PDB; 1UOS; X-ray; A/C=24-157.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   3D-structure; Direct protein sequencing; Glycoprotein; Lectin; Signal.
FT   SIGNAL       1     23
FT   CHAIN       24    158       Convulxin alpha.
FT   DOMAIN      34    158       C-type lectin.
FT   DISULFID    27     38
FT   DISULFID    55    152
FT   DISULFID   104    104       Interchain (with C-100 in beta chain).
FT   DISULFID   127    144
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FT   DISULFID    158    158       Interchain (with C-26 in beta chain).
SQ   SEQUENCE   158 AA;  18141 MW;  949F9C6D673E2318 CRC64;

  Query Match             42.2%;  Score 293.5;  DB 1;  Length 158;
  Best Local Similarity   43.1%;  Pred. No. 5.4e-23;
  Matches   56;  Conservative   27;  Mismatches   38;  Indels    9;  Gaps    2;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              | ||| |   |::||: | :|| |  || ||::|||| ||:|:::| || ||  ::  |
Db         25 LHCPSDWYYYDQHCYRIFNEEMNWEDAEWFCTKQAKGAHLVSIKSAKEADFVAWMVTQNI 84

Qy         62 EYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVDC 112
              |    :: |||||||| : |       ||:||:||:| :  :| :: ::|  |:||   |
Db         85 EESFSHVSIGLRVQNKEKQCSTKWSDGSSVSYDNLLDLYITKCSLLKKETGFRKWFVASC 144

Qy        113 EQQHSFICKF 122
                :  |:|||
Db        145 IGKIPFVCKF 154


RESULT 29
Q9DG39
ID   Q9DG39      PRELIMINARY;      PRT;   152 AA.
AC   Q9DG39;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Halyxin A-chain precursor.
GN   Name=HXNA;
OS   Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
OS   pallas).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Gloydius.
OX   NCBI_TaxID=8714;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF190827; AAG17178.1; -.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Signal.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        24    152       halyxin A-chain.
SQ   SEQUENCE   152 AA;  17455 MW;  BDD74D1DC280C28D CRC64;

  Query Match             42.1%;  Score 292.5;  DB 2;  Length 152;
  Best Local Similarity   41.4%;  Pred. No. 6.6e-23;
  Matches   53;  Conservative   27;  Mismatches   39;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|||||| : :||  |   ||| ||||| :| || ||:|:|:: || ||  ::  | :
Db         24 DCPSGWSSYEGHCYNIFHLFKTWAEAERFCRKQVKGAHLVSIESSEEADFVAQLVSENMK 83

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVDCE 113
                 ||||||||: | : |       ||:||:| ::     |  : ::|  |:|| : |
Db         84 RYGIYIWIGLRVRGKKKQCSSQWSDGSSVSYQNWIEAESKTCLGLQKETEFRKWFNIYCG 143

Qy        114 QQHSFICK 121
              ::: |:|:
Db        144 ERNPFVCE 151


RESULT 30
Q8JIW0
ID   Q8JIW0      PRELIMINARY;      PRT;   152 AA.
AC   Q8JIW0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ACF 1/2 A-chain.
OS   Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Deinagkistrodon.
OX   NCBI_TaxID=36307;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yu H., Xiang K., Wang Y., Liu J.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY091758; AAM22786.1; -.
DR   PIR; JC7134; JC7134.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   152 AA;  17108 MW;  B0870F3DA0A4D23B CRC64;

  Query Match             41.5%;  Score 288.5;  DB 2;  Length 152;
  Best Local Similarity   43.0%;  Pred. No. 1.8e-22;
  Matches   55;  Conservative   24;  Mismatches   40;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :| | ||| : :||| |||  ||| || ||::|  ||||:|:|:: || || :::    :
Db         24 DCSSSWSSYEGHCYKAFKQSKTWADAESFCTKQVNGGHLVSIESSGEADFVAHLIAQKIK 83

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                ::||||| ||| : |       |||||| :  :  :|  | : |  |:|    ||
Db         84 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISYENWIEEESKKCLGVHKATGFRKWENFYCE 143

Qy        114 QQHSFICK 121
                |:  |:|:
Db        144 QRDPFVCE 151


RESULT 31
Q9DEF9
ID   Q9DEF9      PRELIMINARY;      PRT;   152 AA.
AC   Q9DEF9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anticoagulant protein A precursor.
GN   Name=acp-a;
OS   Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Deinagkistrodon.
OX   NCBI_TaxID=36307;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=22167433; PubMed=12175618; DOI=10.1016/S0041-0101(01)00289-6;
RA   Tani A., Ogawa T., Nose T., Nikandrov N.N., Deshimaru M., Chijiwa T.,
RA   Chang C.C., Fukumaki Y., Ohno M.;
RT   "Characterization, primary structure and molecular evolution of
RT   anticoagulant protein from Agkistrodon actus venom.";
RL   Toxicon 40:803-813(2002).
DR   EMBL; AB036880; BAA99281.1; -.
DR   PIR; JC7134; JC7134.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
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DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Signal.
FT   SIGNAL       1     23       Potential.
SQ   SEQUENCE   152 AA;  17124 MW;  5C59C0F503A4D223 CRC64;

  Query Match             41.5%;  Score 288.5;  DB 2;  Length 152;
  Best Local Similarity   43.0%;  Pred. No. 1.8e-22;
  Matches   55;  Conservative   24;  Mismatches   40;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :| | ||| : :||| |||  ||| || ||::|  ||||:|:|:: || || :::    :
Db         24 DCSSSWSSYEGHCYKAFKQSKTWADAESFCTKQVNGGHLVSIESSGEADFVAHLIAQKIK 83

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                ::||||| ||| : |       ||||||| :  :  :|  | : |  |:|    ||
Db         84 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISYENWIEEESKKCLGVHKATGFRKWENFYCE 143

Qy        114 QQHSFICK 121
                |:  |:|:
Db        144 QRDPFVCE 151


RESULT 32
Q9I841
ID   Q9I841      PRELIMINARY;      PRT;   136 AA.
AC   Q9I841;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Aggretin alpha chain (Fragment).
OS   Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Calloselasma.
OX   NCBI_TaxID=8717;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=99443731; PubMed=10512747; DOI=10.1006/bbrc.1999.1457;
RA   Chung C.H., Au L.C., Huang T.F.;
RT   "Molecular cloning and sequence analysis of aggretin, a collagen-like
RT   platelet aggregation inducer.";
RL   Biochem. Biophys. Res. Commun. 263:723-727(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Chung C.H., Au L.C., Huang T.F.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF244900; AAF79952.1; -.
DR   PIR; PC7027; PC7027.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
FT   NON_TER      1      1
FT   NON_TER    136    136
SQ   SEQUENCE   136 AA;  15796 MW;  3B474A4149F0027A CRC64;

  Query Match             41.4%;  Score 288;  DB 2;  Length 136;
  Best Local Similarity   43.8%;  Pred. No. 1.8e-22;
  Matches   57;  Conservative   21;  Mismatches   40;  Indels   12;  Gaps    4;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|  |||  |::||: | :: ||  ||:||  |  | || |:|:  || || : | : |:
Db          4 DCDFGWSPYDQHCYQAFNEQKTWDEAEKFCRAQENGAHLASIESNGEADFV-SWLISQKD 62

Qy         63 YLT--RYIWIGLRVQNKGQPC-------SSISYENLVD--PFECFMVSRDTRLREWFKVD 111
                |    |:||||| ||| | |       ||:|||||:|    :|  : : |  |:|
Db         63 ELADEDYVWIGLRAQNKEQQCSSEWSDGSSVSYENLIDLHTKKCGALEKLTGFRKWVNYY 122

Qy        112 CEQQHSFICK 121
                ||| |:|:||
Db        123 CEQMHAFVCK 132


RESULT 33
Q9IAM1
ID   Q9IAM1      PRELIMINARY;      PRT;   152 AA.
AC   Q9IAM1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Agkisacutacin A chain.
OS   Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Deinagkistrodon.
OX   NCBI_TaxID=36307;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom;
RA   Yu H.-X., Xiang K.-J., Liu J.;
RT   "cDNA sequencing and analysis of eleven C-type lectin-like protein
RT   subunits from Agkistrodon acutus.";
RL   Acta Biochim. Biophys. Sin. 0:0-0(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom;
RA   Cheng X., Qian Y., Liu Q., Li B.X.Y., Ding J., Xu Z., Huang W.,
RA   Liu J.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom;
RA   Yu H.-X., Xiang K.-J., Wang Y., Liu J.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF176420; AAF26286.2; -.
DR   PIR; JC7134; JC7134.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   152 AA;  17109 MW;  76A0F636DBF0D7AB CRC64;

  Query Match             41.4%;  Score 287.5;  DB 2;  Length 152;
  Best Local Similarity   43.0%;  Pred. No. 2.2e-22;
  Matches   55;  Conservative   22;  Mismatches   42;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :| ||||| : :||| |||  ||  || ||::|  ||||:|:|:: || ||  ::    :
Db         24 DCSSGWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 83

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                ::||||| ||| : |       ||||||| :  :  :|  |  :|   :|    ||
Db         84 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISYENWIEEESKKCLGVHIETGFHKWENFYCE 143

Qy        114 QQHSFICK 121
                ||  |:|:
Db        144 QQDPFVCE 151
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RESULT 34
Q71RR4
ID   Q71RR4      PRELIMINARY;      PRT;   152 AA.
AC   Q71RR4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Factor IX/X binding protein alpha chain.
OS   Trimeresurus stejnegeri (Chinese green tree viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=39682;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Lee W.-H., Liu H., Zhang Y.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF354911; AAQ15153.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   152 AA;  17092 MW;  2E355C53C01E243A CRC64;

  Query Match             39.6%;  Score 275.5;  DB 2;  Length 152;
  Best Local Similarity   40.6%;  Pred. No. 4.2e-21;
  Matches   52;  Conservative   25;  Mismatches   42;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :| ||||| : :||| |:    ||  || || |  |||||:|:|:: || ||  ::  | :
Db         24 DCLSGWSSYEGHCYKAFELYKTWEDAESFCMEGVKGGHLVSIESSGEADFVAQLISENMK 83

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVDCE 113
               | ::|||||||    : |       ||:|||| ::     |  : : |: |:|  : |
Db         84 RLDPFVWIGLRVQGDEKQCNSEWSDGSSVSYENWIESESKTCLGLEQQTKFRKWVNLYCG 143

Qy        114 QQHSFICK 121
                |:  |:|:
Db        144 QRIPFVCE 151


RESULT 35
Q696W1
ID   Q696W1      PRELIMINARY;      PRT;   158 AA.
AC   Q696W1;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Factor X activator light chain 2.
OS   Vipera lebetina (Elephant snake) (Leventine viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Macrovipera.
OX   NCBI_TaxID=8709;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Siigur E., Aaspollu A., Trummal K., Tonismaegi K., Tammiste I.,
RA   Kalkkinen N., Siigur J.;
RT   "Factor X activator from Vipera lebetina venom is synthesized from
RT   different genes.";
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY578116; AAT91068.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   158 AA;  18093 MW;  B1E628633627A015 CRC64;

  Query Match             39.4%;  Score 273.5;  DB 2;  Length 158;
  Best Local Similarity   39.5%;  Pred. No. 7.1e-21;
  Matches   51;  Conservative   27;  Mismatches   42;  Indels    9;  Gaps    2;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              |:||   |    :||: ||::  || |||||:|:   |||:|:|:  || ||  :|
Db         25 LDCPPDSSPYRYFCYRVFKEQKNWADAERFCAERPNNGHLVSIESMEEAEFVAQLLSKIT 84

Qy         62 EYLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDC 112
                 : |||||:::| | |       ||:||:||:  :  :|| : : |  | || ::|
Db         85 GKFITHFWIGLRIEDKKQQCRSEWSDGSSVSYDNLLKREFRKCFGLEKGTGYRSWFNLNC 144

Qy        113 EQQHSFICK 121
                |: : |:||
Db        145 EEPYPFVCK 153


RESULT 36
Q7SZV0
ID   Q7SZV0      PRELIMINARY;      PRT;   121 AA.
AC   Q7SZV0;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Factor IX binding protein A chain (Coagulation factor IX-binding
DE   protein chain A) (Fragment).
OS   Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys
OS   pallas).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Gloydius.
OX   NCBI_TaxID=8714;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Zang J., Teng M., Niu L.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY356354; AAQ18640.1; -.
DR   EMBL; AY346127; AAQ24215.1; -.
DR   HSSP; P23806; 1J34.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   121 AA;  13883 MW;  FF7C84DD6A4E4765 CRC64;

  Query Match             38.6%;  Score 268.5;  DB 2;  Length 121;
  Best Local Similarity   41.9%;  Pred. No. 1.8e-20;
  Matches   49;  Conservative   25;  Mismatches   34;  Indels    9;  Gaps    2;

Qy         14 YCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEYLTRYIWIGLR 73
              :||: ||   ||| || ||:|||||||:|:|:  || ||  ::  | :    |:|:|||
Db          4 HCYQTFKLFKTWADAESFCTEQAKGGHLVSIESDGEADFVAQLVAENIQKTEIYVWVGLR 63

Qy         74 VQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVDCEQQHSFICK 121
              || | | |       ||:||:| ::     |  : ::|  |:|| : | ::: |:|:
Db         64 VQGKEQQCSSEWSDGSSVSYQNWIEAESKTCLGLQKETEFRKWFNIYCGERNPFVCE 120


RESULT 37
Q7T248
ID   Q7T248      PRELIMINARY;      PRT;   131 AA.
AC   Q7T248;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Echicetin A-chain.
```

```
OS   Echis carinatus (Saw-scaled viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Echis.
OX   NCBI_TaxID=40353;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   PubMed=14659748; DOI=10.1016/j.jmb.2003.10.048;
RA   Jasti J., Paramasivam M., Srinivasan A., Singh T.P.;
RT   "Crystal structure of echicetin from Echis carinatus (Indian saw-
RT   scaled viper) at 2.4A resolution.";
RL   J. Mol. Biol. 335:167-176(2004).
DR   EMBL; AY268947; AAP41218.2; -.
DR   PDB; 1OZ7; X-ray; A=1-131.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   131 AA;  15363 MW;  F25BEF60AAE7C002 CRC64;

  Query Match             38.2%;  Score 265.5;  DB 2;  Length 131;
  Best Local Similarity   42.1%;  Pred. No. 4.1e-20;
  Matches   56;  Conservative   16;  Mismatches   48;  Indels   13;  Gaps    3;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN--K 61
              || ||||   |||  ||:  ||  ||:||::| | |||||:|:  |   || |:  |  |
Db          2 CPPGWSSNGVYCYMLFKEPKTWDEAEKFCNKQGKDGHLLSIESKKEEILVDIVVSENIGK 61

Qy         62 EYLTRYIWIGLRVQNKGQPCSS--------ISYENLVDPFECFMVSRDTRLREWFKVDCE 113
                |    || ||  ::| | |||         |||  :   |||:: : :  | |    ||
Db         62 MY---KIWTGLSERSKEQHCSSRWSDGSFFRSYEIAIRYSECFVLEKQSVFRTWVATPCE 118

Qy        114 QQHSFICKFTRPR 126
                |:||:  ||
Db        119 NTFPFMCKYPVPR 131


RESULT 38
Q6T7B6
ID   Q6T7B6      PRELIMINARY;      PRT;   156 AA.
AC   Q6T7B6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   C-type lectin-2.
OS   Bitis gabonica (Gaboon adder) (Gaboon viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Bitis.
OX   NCBI_TaxID=8694;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Francischetti I.M.B., Pham V.M., Garfield M.K., Harrison J.,
RA   Ribeiro J.M.C.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY429478; AAR06852.1; -.
DR   HSSP; Q96QQ4; 1K9I.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Lectin.
SQ   SEQUENCE   156 AA;  18157 MW;  1A50D1795904C5B2 CRC64;

  Query Match             37.7%;  Score 262;  DB 2;  Length 156;
  Best Local Similarity   37.0%;  Pred. No. 1.2e-19;
  Matches   50;  Conservative   26;  Mismatches   49;  Indels   10;  Gaps    3;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | |||| |   |::||: | :    | ||:|||||   |||:|:::  || ||  ::  |
Db         22 DFECPSEWRPFDQHCYRAFDEPKRSADAEKFCSEQGNSGHLVSIQSKEEADFVAQLISDN 81

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
               :    |:|:||  | : | |       |:: |:|: : |   || : ::|  | |  :
Db         82 IKSSPDYVWMGLWNQRREQYCSRKWTDGSNVIYKNVAERFTKNCFGLEKETEYRTWLNIL 141

Qy        112 CEQQHSFICKFTRPR 126
                |   : |:|||  ||
Db        142 CGDDYPFVCKFP-PR 155


RESULT 39
ECHA_ECHCA
ID   ECHA_ECHCA     STANDARD;      PRT;   133 AA.
AC   P81017;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Echicetin alpha subunit.
OS   Echis carinatus (Saw-scaled viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Echis.
OX   NCBI_TaxID=40353;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=97250657; PubMed=9163349;
RA   Polgar J., Magnenat E.M., Peitsch M.C., Wells T.N.C., Saqi M.S.A.,
RA   Clemetson K.J.;
RT   "Amino acid sequence of the alpha subunit and computer modelling of
RT   the alpha and beta subunits of echicetin from the venom of Echis
RT   carinatus (saw-scaled viper).";
RL   Biochem. J. 323:533-537(1997).
RN   [2]
RP   CHARACTERIZATION.
RC   TISSUE=Venom;
RX   MEDLINE=93244424; PubMed=8481512;
RA   Peng M., Lu W., Beviglia L., Niewiarowski S., Kirby E.P.;
RT   "Echicetin: a snake venom protein that inhibits binding of von
RT   Willebrand factor and alboaggregins to platelet glycoprotein Ib.";
RL   Blood 81:2321-2328(1993).
CC   -!- FUNCTION: Binds to platelet GPIb and inhibits platelet
CC       agglutination.
CC   -!- SUBUNIT: Heterodimer of alpha and beta subunits.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR   HSSP; P23806; 1J34.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Direct protein sequencing; Lectin.
FT   DISULFID      4     15       By similarity.
FT   DISULFID     31    127       By similarity.
FT   DISULFID    102    119       By similarity.
FT   DISULFID     81     81       Interchain (with C-75 in beta chain) (By
FT                                similarity).
SQ   SEQUENCE   133 AA;  15803 MW;  8F11C2D0BDC70B16 CRC64;

  Query Match             36.9%;  Score 256.5;  DB 1;  Length 133;
  Best Local Similarity   37.8%;  Pred. No. 3.7e-19;
  Matches   51;  Conservative   30;  Mismatches   43;  Indels   11;  Gaps    4;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :| ||||  : :||: |: : ||  ||::|: |  ||||:|:|:  :| ||  ::
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```
Db          1 DQDCLSGWSFYEGHCYQLFRLK-TWDEAEKYCN-QWDGGHLVSIESNAKAEFVAQLISRK 58

Qy         61 --KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKVD 111
                 |  :   :|||| ::| : |       | : ||::| | :||:: | |  |:|  |:
Db         59 LPKSAIEDRVWIGLRDRSKREQCGHLWTDNSFVHYEHVVPPTKCFVLERQTEFRKWIAVN 118

Qy        112 CEQQHSFICKFTRPR 126
               || :  |:||   ||
Db        119 CEFKFPFVCKAKIPR 133


RESULT 40
Q8AYA4
ID   Q8AYA4      PRELIMINARY;      PRT;   146 AA.
AC   Q8AYA4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Agglucetin-beta 1 subunit precursor.
OS   Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Deinagkistrodon.
OX   NCBI_TaxID=36307;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21542539; PubMed=11686327;
RA   Wang W.J., Huang T.F.;
RT   "A novel tetrameric venom protein, agglucetin from Agkistrodon acutus,
RT   acts as a glycoprotein Ib agonist.";
RL   Thromb. Haemost. 86:1077-1086(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22839357; PubMed=12958616;
RA   Wang W.-J., Ling Q.-D., Liau M.-Y., Huang T.-F.;
RT   "A tetrameric glycoprotein Ib-binding protein, agglucetin, from
RT   Formosan pit viper: structure and interaction with human platelets.";
RL   Thromb. Haemost. 90:465-475(2003).
DR   EMBL; AF540647; AAN23126.1; -.
DR   HSSP; O93427; 1UMR.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Signal.
FT   SIGNAL       1     23       Potential.
FT   CHAIN       24    146       agglucetin-beta 1 subunit.
SQ   SEQUENCE   146 AA;  16728 MW;  2342BAE38EB0CCB9 CRC64;

  Query Match             36.8%;  Score 255.5;  DB 2;  Length 146;
  Best Local Similarity   43.2%;  Pred. No. 5.3e-19;
  Matches   54;  Conservative   20;  Mismatches   42;  Indels    9;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| : :||| |||  ||| ||:||::| || || |  :: || ||  |
Db         24 DCPSEWSSYEGHCYKAFKQSKTWADAEKFCTQQHKGSHLASFHSSEEADFV--VTLTTPS 81

Qy         63 YLTRYIWIGLR-VQN----KGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHS 117
                |  :||||: : |    |    : : |::  : ||| :||| |   ||  :||   :|
Db         82 LKTDLVWIGLKNIWNGCYWKWSDGTKLDYKDWREQFEC-LVSR-TVNNEWLSMDCGTTYS 139

Qy        118 FICKF 122
               |:|||
Db        140 FVCKF 144


RESULT 41
ABA4_TRIAB
ID   ABA4_TRIAB     STANDARD;      PRT;   123 AA.
AC   P81114;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Alboaggregin A subunit 4.
OS   Trimeresurus albolabris (White-lipped pit viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=8765;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Venom;
RX   MEDLINE=98189535; PubMed=9531050;
RA   Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA   Calvete J.J., Niewiarowski S.;
RT   "Alboaggregins A and B. Structure and interaction with human
RT   platelets.";
RL   Thromb. Haemost. 79:609-613(1998).
CC   -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC       agglutination.
CC   -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4, disulfide-
CC       linked.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR   HSSP; P22030; 1IJK.
DR   InterPro; IPR002353; AntifreezeII.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR00356; ANTIFREEZEII.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Direct protein sequencing; Lectin.
FT   DOMAIN       1    123       C-type lectin.
FT   DISULFID     2     13       By similarity.
FT   DISULFID    30    119       By similarity.
FT   DISULFID    96    111       By similarity.
SQ   SEQUENCE   123 AA;  14365 MW;  D4CFBEE1219C9B1E CRC64;

  Query Match             36.3%;  Score 252.5;  DB 1;  Length 123;
  Best Local Similarity   39.7%;  Pred. No. 9e-19;
  Matches   52;  Conservative   22;  Mismatches   36;  Indels   21;  Gaps    6;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDN----VLY 58
              :||| ||| : :||: | :   || ||:||::| || ||:| ::: || ||      :|
Db          1 DCPSDWSSYEGHCYRVFNEPQNWADAEKFCTQQHKGSHLVSFQSSEEADFVVQMTRPILN 60

Qy         59 ANKEYLTRYIWIGLRVQNKGQPCSS-------ISYENLVDPFECFMVSRDTRLREWFKVD 111
              ||       :||||    |    |:|       : |:   : ||| :||| |   ||  :|
Db         61 AN------LVWIGL--SNLWNQCNSQWSDGTXLDYKXWREQFEC-LVSRTTN-NEWLSMD 110

Qy        112 CEQQHSFICKF 122
               |   |||:|:|
Db        111 CSSTHSFVCEF 121


RESULT 42
Q6X5T3
ID   Q6X5T3      PRELIMINARY;      PRT;   152 AA.
AC   Q6X5T3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   C-type lectin CTL-5 (Fragment).
OS   Bitis arietans (African puff adder).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Bitis.
OX   NCBI_TaxID=8692;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Harrison R.A., Oliver J.L., Hasson S.S., Theakston D.R.D.G.;
```

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RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY254327; AAQ01208.1; -.
DR   HSSP; Q9H8F0; 1K9J.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Lectin.
FT   NON_TER     152    152
SQ   SEQUENCE   152 AA;  17254 MW;  78AB99D138108149 CRC64;

  Query Match             36.2%;  Score 251.5;  DB 2;  Length 152;
  Best Local Similarity   36.9%;  Pred. No. 1.5e-18;
  Matches   48;  Conservative   27;  Mismatches   42;  Indels   13;  Gaps    3;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :||| ||:  ::||: || | :|| ||:|| |||  |||:|:::  ||:||  ::
Db         24 DFQCPSEWSAYGQHCYRAFKYEKSWAEAEKFCMEQANDGHLVSIQSIKEANFVAKLVSG- 82

Qy         61 KEYLTRYIWIGLRVQNKGQPCSS-------ISYENLVDPFE--CFMVSRDTRLREWFKVD 111
                 :  ||||||| : | | |:|       ::| |  :     | :::  :  : |   |
Db         83 ---IIAYIWIGLRDRRKEQQCTSEWNDGSKVTYVNWREGESQMCQVLAIWSGFKNWVNTD 139

Qy        112 CEQQHSFICK 121
                |   : |:||
Db        140 CASHNPFVCK 149


RESULT 43
Q9IAM0
ID   Q9IAM0      PRELIMINARY;      PRT;   146 AA.
AC   Q9IAM0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Agkisacutacin B chain.
OS   Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Deinagkistrodon.
OX   NCBI_TaxID=36307;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom;
RA   Cheng X., Qian Y., Liu Q., Li B.X.Y., Ding J., Xu Z., Huang W.,
RA   Liu J.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF176421; AAF26287.1; -.
DR   HSSP; P22030; 1IJK.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   146 AA;  16726 MW;  7360B6D6864131BB CRC64;

  Query Match             35.9%;  Score 249.5;  DB 2;  Length 146;
  Best Local Similarity   42.4%;  Pred. No. 2.3e-18;
  Matches   53;  Conservative   20;  Mismatches   43;  Indels    9;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| : :|||||  :  ||| ||:||::| || || |  :: || ||  |
Db         24 DCPSDWSSYEGHCYKPFDEPKTWADAEKFCTQQHKGSHLASFHSSEEADFV--VTLTTPS 81

Qy         63 YLTRYIWIGLR-VQN----KGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHS 117
                 |  :|||: : |    |    : : |::  : ||| :||| |   ||  :||    |
Db         82 LKTDLVWIGLKNIWNGCYWKWSDGTKLDYKDWREQFEC-LVSR-TVNNEWLSMDCGTTCS 139

Qy        118 FICKF 122
                |:|||
Db        140 FVCKF 144


RESULT 44
CVXB_CRODU
ID   CVXB_CRODU     STANDARD;      PRT;   148 AA.
AC   O93427;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Convulxin beta precursor (CVX beta).
OS   Crotalus durissus terrificus (South American rattlesnake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Crotalus.
OX   NCBI_TaxID=8732;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
RC   TISSUE=Venom gland;
RX   MEDLINE=98324901; PubMed=9657980;
RA   Leduc M., Bon C.;
RT   "Cloning of subunits of convulxin, a collagen-like platelet-
RT   aggregating protein from Crotalus durissus terrificus venom.";
RL   Biochem. J. 333:389-393(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Radis-Baptista G., Camargo A.C.M., Yamane T.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 24-148.
RX   PubMed=14521935; DOI=10.1016/j.bbrc.2003.09.032;
RA   Murakami M.T., Zela S.P., Gava L.M., Michelan-Duarte S.,
RA   Cintra A.C.O., Arni R.K.;
RT   "Crystal structure of the platelet activator convulxin, a disulfide-
RT   linked alpha4beta4 cyclic tetramer from the venom of Crotalus durissus
RT   terrificus.";
RL   Biochem. Biophys. Res. Commun. 310:478-482(2003).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 25-148.
RX   PubMed=14684891;
RA   Batuwangala T., Leduc M., Gibbins J.M., Bon C., Jones E.Y.;
RT   "Structure of the snake-venom toxin convulxin.";
RL   Acta Crystallogr. D 60:46-53(2004).
CC   -!- FUNCTION: Binds to the platelet and collagen receptor,
CC       glycoprotein VI (GPVI).
CC   -!- SUBUNIT: Heterooctamer of four alpha chains and four beta chains;
CC       disulfide-linked.
CC   -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y16349; CAA76182.1; -.
DR   EMBL; AF541881; AAQ11362.1; -.
DR   PDB; 1UMR; X-ray; C/D=24-148.
DR   PDB; 1UOS; X-ray; B/D=23-148.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   3D-structure; Direct protein sequencing; Glycoprotein; Lectin; Signal.
```

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FT   SIGNAL       1     23
FT   CHAIN       24    148       Convulxin beta.
FT   DOMAIN      34    148       C-type lectin.
FT   DISULFID    26     26       Interchain (with C-158 in alpha chain).
FT   DISULFID    27     38
FT   DISULFID    55    144
FT   DISULFID   100    100       Interchain (with C-104 in alpha chain).
FT   DISULFID   121    136
FT   CONFLICT   113    113       K -> E (in Ref. 2).
FT   CONFLICT   148    148       A -> V (in Ref. 2).
SQ   SEQUENCE   148 AA;  17402 MW;  94D7E3E1BC693B9F CRC64;

  Query Match             35.9%;  Score 249.5;  DB 1;  Length 148;
  Best Local Similarity   41.3%;  Pred. No. 2.3e-18;
  Matches   52;  Conservative   17;  Mismatches   44;  Indels   13;  Gaps    5;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              ||| ||| |||||| |||||||| ||:||::|  | ||:|  :  |  ||  |   ::
Db         27 CPSHWSSYDRYCYKVFKQEMTWADAEKFCTQQHTGSHLVSFHSTEEVDFV--VKMTHQSL 84

Qy         64 LTRYIWIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKVDCEQQH 116
               : : |||   |  |       :   |:   : ||| ::|| |   :|    |   :
Db         85 KSTFFWIG--ANNIWNKCNWQWSDGTKPEYKEWHEEFEC-LISR-TFDNQWLSAPCSDTY 140

Qy        117 SFICKF 122
              ||:|||
Db        141 SFVCKF 146


RESULT 45
Q8JIW1
ID   Q8JIW1      PRELIMINARY;      PRT;   146 AA.
AC   Q8JIW1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Agkisacutacin B-chain.
OS   Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Deinagkistrodon.
OX   NCBI_TaxID=36307;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yu H., Xiang K., Wang Y., Liu J.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY091756; AAM22785.1; -.
DR   PIR; JC7135; JC7135.
DR   HSSP; O93427; 1UMR.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   146 AA;  16740 MW;  6260B6D68741317C CRC64;

  Query Match             35.8%;  Score 248.5;  DB 2;  Length 146;
  Best Local Similarity   42.4%;  Pred. No. 2.9e-18;
  Matches   53;  Conservative   20;  Mismatches   43;  Indels    9;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| : :||||| :  ||| ||:||::| || || |  :: || ||  |
Db         24 DCPSEWSSYEGHCYKPFDEPKTWADAEKFCTQQHKGSHLASFHSSEEADFV--VTLTTPS 81

Qy         63 YLTRYIWIGLR-VQN----KGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHS 117
                 |  :||||: : |    |   : : |::  : ||| :||| |   ||  :||   |
Db         82 LKTDLVWIGLKNIWNGCYWKWSDGTKLDYKDWREQFEC-LVSR-TVNNEWLSMDCGTTCS 139

Qy        118 FICKF 122
              |:|||
Db        140 FVCKF 144


RESULT 46
Q71RP8
ID   Q71RP8      PRELIMINARY;      PRT;   148 AA.
AC   Q71RP8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Stejaggregin-A beta chain-3.
OS   Trimeresurus stejnegeri (Chinese green tree viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=39682;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Lee W.-H., Liu H., Zhang Y.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF354927; AAQ15169.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   148 AA;  16966 MW;  FBEC0046C3642524 CRC64;

  Query Match             35.5%;  Score 246.5;  DB 2;  Length 148;
  Best Local Similarity   39.7%;  Pred. No. 4.8e-18;
  Matches   50;  Conservative   20;  Mismatches   43;  Indels   13;  Gaps    4;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              || |||| | |||| ||||| |  ||:||:||  | ||:|  :: || || |: |   :
Db         27 CPLGWSSYDLYCYKVFKQEMNWTDAEKFCTEQHTGSHLVSFHSSEEADFVVNMTYPILK- 85

Qy         64 LTRYIWIGLRVQNKGQPCSS-------ISYENLVDPFECFMVSRDTRLREWFKVDCEQQH 116
                 ::||||   |   |:|       ::|::     ||  ::  |   :|:   | : |
Db         86 -LDFVWIGL--SNVWNQCNSEWSDGTKLNYKDWSGESEC--IASKTIENQWWSRSCSRTH 140

Qy        117 SFICKF 122
                :|||
Db        141 YVVCKF 146


RESULT 47
Q6T7B5
ID   Q6T7B5      PRELIMINARY;      PRT;   157 AA.
AC   Q6T7B5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   C-type lectin-3.
OS   Bitis gabonica (Gaboon adder) (Gaboon viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Bitis.
OX   NCBI_TaxID=8694;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Francischetti I.M.B., Pham V.M., Garfield M.K., Harrison J.,
RA   Ribeiro J.M.C.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY429479; AAR06853.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
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DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW   Lectin.
SQ   SEQUENCE   157 AA;  18095 MW;  1A372C788C4BDC62 CRC64;

  Query Match             35.1%;  Score 244;  DB 2;  Length 157;
  Best Local Similarity   36.6%;  Pred. No. 9.4e-18;
  Matches   49;  Conservative   25;  Mismatches   44;  Indels   16;  Gaps    4;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :||| ||:  ::||: |    ||  ||:||:|| | |||:|:::  ||:||  ::
Db         24 DFQCPSEWSAYGQHCYRAFSDLKTWEDAEKFCTEQEKAGHLVSIQSIQEANFVAQLV--- 80

Qy         61 KEYLTR----YIWIGLRVQNKGQPCSS-------ISYENLVDPFE--CFMVSRDTRLREW 107
                :::     ||||||| : | | |||       : | |  :     |  ::: |   :|
Db         81 SGFISGSPKIYIWIGLRDRRKEQQCSSEWNDGSKVIYVNWREGESQMCQALTKWTEFHQW 140

Qy        108 FKVDCEQQHSFICK 121
                ||   : ||||
Db        141 LNTDCAGHYPFICK 154


RESULT 48
Q7T2Q1
ID   Q7T2Q1      PRELIMINARY;      PRT;   157 AA.
AC   Q7T2Q1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   EMS16 A chain.
OS   Echis multisquamatus (Central Asian sand viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Echis.
OX   NCBI_TaxID=93050;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22825200; PubMed=12944366;
RA   Okuda D., Horii K., Mizuno H., Morita T.;
RT   "Characterization and preliminary crystallographic studies of EMS16,
RT   an antagonist of collagen receptor (GPIa/IIa) from the venom of Echis
RT   multisquamatus.";
RL   J. Biochem. 134:19-23(2003).
DR   EMBL; AB098253; BAC77706.1; -.
DR   PDB; 1UKM; X-ray; A=24-157.
DR   PDB; 1V7P; X-ray; A=-.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   157 AA;  18214 MW;  F0D9638C6D622AB3 CRC64;

  Query Match             35.0%;  Score 243.5;  DB 2;  Length 157;
  Best Local Similarity   34.8%;  Pred. No. 1.1e-17;
  Matches   46;  Conservative   27;  Mismatches   50;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :||| |:: |::||    :   |  |||||:|||| |||:|:::  | :||  ::
Db         24 DFDCPSDWTAYDQHCYLAIGEPQNWYEAERFCTEQAKDGHLVSIQSREEGNFVAQLVSGF 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVD 111
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Db         84 MHRSEIYVWIGLRDRREEQQCNPEWNDGSKIIYVNWKEGESKMCQGLTKWTNFHDWNNIN 143

Qy        112 CEQQHSFICKFT 123
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Db        144 CEDLYPFVCKFS 155


RESULT 49
Q7LZK5
ID   Q7LZK5      PRELIMINARY;      PRT;   131 AA.
AC   Q7LZK5;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Bitiscetin alpha chain.
OS   Bitis arietans (African puff adder).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Viperinae; Bitis.
OX   NCBI_TaxID=8692;
RN   [1]
RP   SEQUENCE.
RA   Matsui T., Hamako J., Suzuki M., Hayashi N., Ito M., Makita K.,
RA   Fujimura Y., Ozeki Y., Titani K.;
RL   Submitted (JAN-1997) to the PIR data bank.
RN   [2]
RP   SEQUENCE.
RA   Matsui T., Hamako J., Suzuki M., Hayashi N., Ito M., Makita K.,
RA   Fujimura Y., Ozeki Y., Titani K.;
RT   "Complete amino acid sequence of bitiscetin, a novel von Willebrand
RT   factor modulator protein purified from snake venom of Bitis
RT   arietans.";
RL   Biochem. Cell Biol. 1:271-284(1997).
DR   PIR; JC5058; JC5058.
DR   HSSP; P22030; 1IJK.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR002353; AntifreezeII.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR00356; ANTIFREEZEII.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   131 AA;  14935 MW;  29592D3A0C05D521 CRC64;

  Query Match             34.9%;  Score 242.5;  DB 2;  Length 131;
  Best Local Similarity   38.5%;  Pred. No. 1.1e-17;
  Matches   52;  Conservative   23;  Mismatches   45;  Indels   15;  Gaps    4;

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Db          1 DPGCLPDWSSYKGHCYKVFKKVGTWEDAEKFCVENS--GHLASIDSKEEADFVTKLA--- 55

Qy         61 KEYLTRYI---WIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKV 110
               : ||:::   ||||| ::| | |        ||: |||: :| :|| :   |  | |  :
Db         56 SQTLTKFVYDAWIGLRDESKTQQCSPQWTDGSSVVYENVDEPTKCFGLDVHTEYRTWTDL 115

Qy        111 DCEQQHSFICKFTRP 125
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Db        116 PCGEKNPFICKSRLP 130


RESULT 50
Q71RP9
ID   Q71RP9      PRELIMINARY;      PRT;   148 AA.
AC   Q71RP9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Stejaggregin-A beta chain-2.
OS   Trimeresurus stejnegeri (Chinese green tree viper).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Trimeresurus.
OX   NCBI_TaxID=39682;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RA   Lee W.-H., Liu H., Zhang Y.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF354926; AAQ15168.1; -.
DR   HSSP; Q9H8F0; 1K9J.
DR   GO; GO:0005529; F:sugar binding; IEA.
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DR   InterPro; IPR001304; Lectin_C.
DR   InterPro; IPR003990; Pancreatis_ac.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PRINTS; PR01504; PNCREATITSAP.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   148 AA;  16936 MW;  E49BBCAA03AAA53F CRC64;

  Query Match             34.9%;  Score 242.5;  DB 2;  Length 148;
  Best Local Similarity   38.9%;  Pred. No. 1.3e-17;
  Matches   49;  Conservative   20;  Mismatches   44;  Indels   13;  Gaps    4;

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Db         27 CPLGWSSYDLYCYKVFKQQMNWTDAEKFCTEQHTGSHLVSFHSSEEADFVVNMTYPILK- 85

Qy         64 LTRYIWIGLRVQNKGQPCSS-------ISYENLVDPFECFMVSRDTRLREWFKVDCEQQH 116
                ::||||   |    |:|       : |::     ||  ::  |   :|:   | : |
Db         86 -LDFVWIGL--SNVWNQCNSEWSDGTKLDYKDWSGESEC--IASKTVENQWWTKSCSRTH 140

Qy        117 SFICKF 122
               :|||
Db        141 YVVCKF 146


Search completed: May  2, 2005, 16:01:51
Job time : 71 secs
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OM protein - protein search, using sw model

Run on: May 2, 2005, 16:01:56 ; Search time 56 Seconds
(without alignments)
749.489 Million cell updates/sec

Title: US-10-749-387-1
Perfect score: 695
Sequence: 1 DLECPSGWSSTDRYCYKPFK.....WFKVDCEQQHSFICKFTRPR 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	695	100.0	126	9	US-09-969-763-1	Sequence 1, Appli
2	695	100.0	126	16	US-10-749-387-1	Sequence 1, Appli
3	684	98.4	149	9	US-09-969-763-3	Sequence 3, Appli
4	684	98.4	149	16	US-10-749-387-3	Sequence 3, Appli
5	542	78.0	110	9	US-09-969-763-10	Sequence 10, Appl
6	542	78.0	110	16	US-10-749-387-10	Sequence 10, Appl
7	361.5	52.0	158	9	US-09-929-230-11	Sequence 11, Appl
8	361.5	52.0	158	14	US-10-226-420-11	Sequence 11, Appl
9	316.5	45.5	144	9	US-09-929-230-8	Sequence 8, Appli
10	316.5	45.5	144	14	US-10-226-420-8	Sequence 8, Appli
11	314.5	45.3	152	9	US-09-929-230-5	Sequence 5, Appli
12	314.5	45.3	152	14	US-10-226-420-5	Sequence 5, Appli
13	271.5	39.1	129	10	US-09-938-114-2	Sequence 2, Appli
14	184.5	26.5	151	9	US-09-929-230-2	Sequence 2, Appli
15	184.5	26.5	151	14	US-10-226-420-2	Sequence 2, Appli
16	168	24.2	166	10	US-09-997-003-30	Sequence 30, Appl
17	168	24.2	166	10	US-09-997-003-43	Sequence 43, Appl
18	168	24.2	166	16	US-10-734-564-2	Sequence 2, Appli
19	168	24.2	166	16	US-10-734-564-4	Sequence 4, Appli
20	168	24.2	174	9	US-09-925-301-1182	Sequence 1182, Ap
21	164.5	23.7	175	15	US-10-028-248A-112	Sequence 112, App
22	164.5	23.7	175	15	US-10-107-782-112	Sequence 112, App
23	157.5	22.7	175	15	US-10-028-248A-111	Sequence 111, App
24	157.5	22.7	175	15	US-10-107-782-111	Sequence 111, App
25	154.5	22.2	175	15	US-10-028-248A-110	Sequence 110, App
26	154.5	22.2	175	15	US-10-107-782-110	Sequence 110, App
27	153.5	22.1	175	14	US-10-316-761-3	Sequence 3, Appli
28	153.5	22.1	175	15	US-10-434-906-1	Sequence 1, Appli
29	153.5	22.1	175	15	US-10-028-248A-109	Sequence 109, App
30	153.5	22.1	175	15	US-10-107-782-109	Sequence 109, App
31	153.5	22.1	183	9	US-09-925-301-1013	Sequence 1013, Ap
32	148.5	21.4	175	9	US-09-978-295A-452	Sequence 452, App
33	148.5	21.4	175	9	US-09-978-697-452	Sequence 452, App
34	148.5	21.4	175	9	US-09-978-192A-452	Sequence 452, App
35	148.5	21.4	175	9	US-09-999-832A-452	Sequence 452, App
36	148.5	21.4	175	10	US-09-978-189-452	Sequence 452, App
37	148.5	21.4	175	10	US-09-978-608A-452	Sequence 452, App
38	148.5	21.4	175	10	US-09-978-585A-452	Sequence 452, App
39	148.5	21.4	175	10	US-09-978-191A-452	Sequence 452, App
40	148.5	21.4	175	10	US-09-978-403A-452	Sequence 452, App
41	148.5	21.4	175	10	US-09-978-564A-452	Sequence 452, App
42	148.5	21.4	175	10	US-09-999-833A-452	Sequence 452, App
43	148.5	21.4	175	10	US-09-981-915A-452	Sequence 452, App
44	148.5	21.4	175	10	US-09-978-824-452	Sequence 452, App
45	148.5	21.4	175	10	US-09-918-585A-452	Sequence 452, App
46	148.5	21.4	175	10	US-09-999-834A-452	Sequence 452, App
47	148.5	21.4	175	10	US-09-978-423A-452	Sequence 452, App
48	148.5	21.4	175	10	US-09-978-193A-452	Sequence 452, App
49	148.5	21.4	175	10	US-09-999-830A-452	Sequence 452, App
50	148.5	21.4	175	10	US-09-978-757A-452	Sequence 452, App
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52	148.5	21.4	175	10	US-09-978-643A-452	Sequence 452, App
53	148.5	21.4	175	10	US-09-978-375A-452	Sequence 452, App
54	148.5	21.4	175	10	US-09-978-298A-452	Sequence 452, App
55	148.5	21.4	175	10	US-09-978-188A-452	Sequence 452, App
56	148.5	21.4	175	10	US-09-978-681A-452	Sequence 452, App
57	148.5	21.4	175	10	US-09-978-194A-452	Sequence 452, App
58	148.5	21.4	175	10	US-09-999-829A-452	Sequence 452, App
59	148.5	21.4	175	10	US-09-978-299A-452	Sequence 452, App
60	148.5	21.4	175	10	US-09-978-544A-452	Sequence 452, App
61	148.5	21.4	175	10	US-09-978-665A-452	Sequence 452, App
62	148.5	21.4	175	10	US-09-978-802A-452	Sequence 452, App
63	148.5	21.4	175	11	US-09-999-831A-452	Sequence 452, App
64	148.5	21.4	175	13	US-10-052-586-424	Sequence 424, App
65	148.5	21.4	175	14	US-10-174-590-424	Sequence 424, App

ALIGNMENTS

RESULT 1
US-09-969-763-1
; Sequence 1, Application US/09969763
; Publication No. US20020198363A1
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOYUKI
; APPLICANT: KITO, MORIKAZU
; APPLICANT: KAYAHARA, TAKASHI
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHKI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING TH
; FILE REFERENCE: 214760US0

; CURRENT APPLICATION NUMBER: US/09/969,763
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Crotallus horridus
US-09-969-763-1

Query Match 100.0%; Score 695; DB 9; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
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Db          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

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Qy        121 KFTRPR 126
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Db        121 KFTRPR 126
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RESULT 2
US-10-749-387-1
; Sequence 1, Application US/10749387
; Publication No. US20040161822A1
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOYUKI
; APPLICANT: KITO, MORIKAZU
; APPLICANT: KAYAHARA, TAKASHI
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHKI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING T
; FILE REFERENCE: 214760US0
; CURRENT APPLICATION NUMBER: US/10/749,387
; CURRENT FILING DATE: 2004-01-02
; PRIOR APPLICATION NUMBER: US/09/969,763
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Crotallus horridus
US-10-749-387-1

Query Match 100.0%; Score 695; DB 16; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126
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RESULT 3
US-09-969-763-3
; Sequence 3, Application US/09969763
; Publication No. US20020198363A1
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOYUKI
; APPLICANT: KITO, MORIKAZU
; APPLICANT: KAYAHARA, TAKASHI
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHKI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING TH
; FILE REFERENCE: 214760US0
; CURRENT APPLICATION NUMBER: US/09/969,763
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Crotalus harridus
US-09-969-763-3

Query Match 98.4%; Score 684; DB 9; Length 149;
Best Local Similarity 98.4%; Pred. No. 7.4e-71;
Matches 124; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
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Qy        121 KFTRPR 126
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Db        144 KFTRPR 149
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RESULT 4
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; Sequence 3, Application US/10749387
; Publication No. US20040161822A1
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOYUKI
; APPLICANT: KITO, MORIKAZU
; APPLICANT: KAYAHARA, TAKASHI
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHKI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING TH
; FILE REFERENCE: 214760US0
; CURRENT APPLICATION NUMBER: US/10/749,387
; CURRENT FILING DATE: 2004-01-02
; PRIOR APPLICATION NUMBER: US/09/969,763
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3

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;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Crotalus harridus
US-10-749-387-3

  Query Match             98.4%;  Score 684;  DB 16;  Length 149;
  Best Local Similarity   98.4%;  Pred. No. 7.4e-71;
  Matches  124;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| |||||||||||||| |||||||||||||||||||||||||||||||||
Db         24 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 143

Qy        121 KFTRPR 126
              ||||||
Db        144 KFTRPR 149


RESULT 5
US-09-969-763-10
; Sequence 10, Application US/09969763
; Publication No. US20020198363A1
; GENERAL INFORMATION:
;  APPLICANT: FUKUCHI, NAOYUKI
;  APPLICANT:  KITO, MORIKAZU
;  APPLICANT:  KAYAHARA, TAKASHI
;  APPLICANT:  FUTAKI, FUMIE
;  APPLICANT:  ISHIKAWA, KOHKI
;  APPLICANT:  SUZUKI, EIICHIRO
;  APPLICANT:  GONDOH, KEIKO
;  APPLICANT:  SHIMBA, NOBUHISA
;  APPLICANT:  YAMADA, NAOYUKI
;  TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING T
;  FILE REFERENCE: 214760US0
;  CURRENT APPLICATION NUMBER: US/09/969,763
;  CURRENT FILING DATE:  2000-10-25
;  PRIOR APPLICATION NUMBER: JP 2000-305279
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-969-763-10

  Query Match             78.0%;  Score 542;  DB 9;  Length 110;
  Best Local Similarity   81.7%;  Pred. No. 1.3e-54;
  Matches  103;  Conservative    1;  Mismatches    6;  Indels   16;  Gaps    1;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              ||||||||||  ||||||||||||:| ||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYSRYCYKPFKQEMTYADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||                  ||||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRFFF---------------FECFMVSRDTRLREWFKVDCEQQHSFIC 104

Qy        121 KFTRPR 126
              ||||||
Db        105 KFTRPR 110


RESULT 6
US-10-749-387-10
; Sequence 10, Application US/10749387
; Publication No. US20040161822A1
; GENERAL INFORMATION:
;  APPLICANT: FUKUCHI, NAOYUKI
;  APPLICANT:  KITO, MORIKAZU
;  APPLICANT:  KAYAHARA, TAKASHI
;  APPLICANT:  FUTAKI, FUMIE
;  APPLICANT:  ISHIKAWA, KOHKI
;  APPLICANT:  SUZUKI, EIICHIRO
;  APPLICANT:  GONDOH, KEIKO
;  APPLICANT:  SHIMBA, NOBUHISA
;  APPLICANT:  YAMADA, NAOYUKI
;  TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING TH
;  FILE REFERENCE: 214760US0
;  CURRENT APPLICATION NUMBER: US/10/749,387
;  CURRENT FILING DATE:  2004-01-02
;  PRIOR APPLICATION NUMBER: US/09/969,763
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: JP 2000-305279
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-749-387-10

  Query Match             78.0%;  Score 542;  DB 16;  Length 110;
  Best Local Similarity   81.7%;  Pred. No. 1.3e-54;
  Matches  103;  Conservative    1;  Mismatches    6;  Indels   16;  Gaps    1;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              ||||||||||  ||||||||||||:| ||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYSRYCYKPFKQEMTYADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||                  ||||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRFFF---------------FECFMVSRDTRLREWFKVDCEQQHSFIC 104

Qy        121 KFTRPR 126
              ||||||
Db        105 KFTRPR 110


RESULT 7
US-09-929-230-11
; Sequence 11, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
;  APPLICANT: Sheppard, Paul O.
;  APPLICANT:  Bishop, Paul D.
;  TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
;  FILE REFERENCE: 00-72
;  CURRENT APPLICATION NUMBER: US/09/929,230
;  CURRENT FILING DATE:  2001-08-13
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 158
;   TYPE: PRT
;   ORGANISM: Sistrurus miliarius
US-09-929-230-11

  Query Match             52.0%;  Score 361.5;  DB 9;  Length 158;
  Best Local Similarity   50.4%;  Pred. No. 1.6e-33;
  Matches   66;  Conservative   21;  Mismatches   35;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  ||||| : |:|||:  |:  ||  |||||||||||||| |||   || |:  :: ||
Db         24 DFNCPSGWFAYDQYCYRVIKRLKTWDDAERFCSEQAKGGHLASVENDEEAVFLAQLVAAN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
```

```
              :    |:|||||:||||| |       ||:||||||     :|| : ::|   :|:  |
Db         84 IKQNQYYVWIGLRIQNKGQQCSTKWSDGSSVSYENLVKSHSKKCFGLKKETEFLQWYNTD 143

Qy        112 CEQQHSFICKF 122
              ||::: |:|||
Db        144 CEEKNLFVCKF 154


RESULT 8
US-10-226-420-11
; Sequence 11, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
;  APPLICANT: Sheppard, Paul O.
;  APPLICANT:  Bishop, Paul D.
;  TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
;  FILE REFERENCE: 00-72
;  CURRENT APPLICATION NUMBER: US/10/226,420
;  CURRENT FILING DATE:  2002-08-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 158
;   TYPE: PRT
;   ORGANISM: Sistrurus miliarius
US-10-226-420-11

  Query Match             52.0%;  Score 361.5;  DB 14;  Length 158;
  Best Local Similarity   50.4%;  Pred. No. 1.6e-33;
  Matches   66;  Conservative   21;  Mismatches   35;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  ||||| : |:|||:  |:  ||  |||||||||||||| |||   || |:  :: ||
Db         24 DFNCPSGWFAYDQYCYRVIKRLKTWDDAERFCSEQAKGGHLASVENDEEAVFLAQLVAAN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
              :    |:|||||:||||| |       ||:||||||     :|| : ::|   :|:  |
Db         84 IKQNQYYVWIGLRIQNKGQQCSTKWSDGSSVSYENLVKSHSKKCFGLKKETEFLQWYNTD 143

Qy        112 CEQQHSFICKF 122
              ||::: |:|||
Db        144 CEEKNLFVCKF 154


RESULT 9
US-09-929-230-8
; Sequence 8, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
;  APPLICANT: Sheppard, Paul O.
;  APPLICANT:  Bishop, Paul D.
;  TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
;  FILE REFERENCE: 00-72
;  CURRENT APPLICATION NUMBER: US/09/929,230
;  CURRENT FILING DATE:  2001-08-13
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Sistrurus miliarius
US-09-929-230-8

  Query Match             45.5%;  Score 316.5;  DB 9;  Length 144;
  Best Local Similarity   45.8%;  Pred. No. 2.3e-28;
  Matches   60;  Conservative   24;  Mismatches   38;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :||| | : |:|||:  ||  ||  |||||||||||||:|:|:  ||:||  ::  |
Db         10 DFDCPSDWYAYDQYCYRVIKQLRTWDDAERFCSEQAKGGHLVSIESDGEAAFVAQLVAEN 69

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVD--PFECFMVSRDTRLREWFKVD 111
              :     :|||||:| : : |       ||::||||:     :|| : ::|  | |  |
```

```
Db         70 IKQNKYDVWIGLRIQGEEKQCSTKWSDGSSVNYENLIKHATKKCFGLKKETGFRTWRNVH 129

Qy        112 CEQQHSFICKF 122
              | ||: |:|||
Db        130 CTQQNLFMCKF 140


RESULT 10
US-10-226-420-8
; Sequence 8, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
;  APPLICANT: Sheppard, Paul O.
;  APPLICANT:  Bishop, Paul D.
;  TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
;  FILE REFERENCE: 00-72
;  CURRENT APPLICATION NUMBER: US/10/226,420
;  CURRENT FILING DATE:  2002-08-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Sistrurus miliarius
US-10-226-420-8

  Query Match             45.5%;  Score 316.5;  DB 14;  Length 144;
  Best Local Similarity   45.8%;  Pred. No. 2.3e-28;
  Matches   60;  Conservative   24;  Mismatches   38;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :||| | : |:|||:  ||  ||  |||||||||||||:|:|:  ||:||  ::  |
Db         10 DFDCPSDWYAYDQYCYRVIKQLRTWDDAERFCSEQAKGGHLVSIESDGEAAFVAQLVAEN 69

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVD--PFECFMVSRDTRLREWFKVD 111
              :     :|||||:| : : |       ||::||||:     :|| : ::|  | |  |
Db         70 IKQNKYDVWIGLRIQGEEKQCSTKWSDGSSVNYENLIKHATKKCFGLKKETGFRTWRNVH 129

Qy        112 CEQQHSFICKF 122
              | ||: |:|||
Db        130 CTQQNLFMCKF 140


RESULT 11
US-09-929-230-5
; Sequence 5, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
;  APPLICANT: Sheppard, Paul O.
;  APPLICANT:  Bishop, Paul D.
;  TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
;  FILE REFERENCE: 00-72
;  CURRENT APPLICATION NUMBER: US/09/929,230
;  CURRENT FILING DATE:  2001-08-13
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 152
;   TYPE: PRT
;   ORGANISM: Sistrurus miliarius
US-09-929-230-5

  Query Match             45.3%;  Score 314.5;  DB 9;  Length 152;
  Best Local Similarity   45.3%;  Pred. No. 4.2e-28;
  Matches   58;  Conservative   25;  Mismatches   36;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||||||| |::||: |||  ||  |||||||||:||||:|:|:: ||:||  ::  |:
Db         24 DCPSGWSSYDQHCYRVFKQLKTWDDAERFCSEQAEGGHLVSIESSEEAAFVAQLVPENRR 83

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVDCE 113
                 |||||||| | : |     ||:|||| ::      |  : : |   :|  : |
Db         84 RAILYIWIGLRVQGKEKQCSAKWSDGSSVSYENWIEAESKTCLGLQQGTNYHKWVNIYCG 143
```

```
Qy        114 QQHSFICK 121
                : : |:|:
Db        144 EINPFVCE 151


RESULT 12
US-10-226-420-5
; Sequence 5, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
;  APPLICANT: Sheppard, Paul O.
;  APPLICANT:  Bishop, Paul D.
;  TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
;  FILE REFERENCE: 00-72
;  CURRENT APPLICATION NUMBER: US/10/226,420
;  CURRENT FILING DATE:  2002-08-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 152
;   TYPE: PRT
;   ORGANISM: Sistrurus miliarius
US-10-226-420-5

  Query Match             45.3%;  Score 314.5;  DB 14;  Length 152;
  Best Local Similarity   45.3%;  Pred. No. 4.2e-28;
  Matches   58;  Conservative   25;  Mismatches   36;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|||||| |::||: ||| || ||||||||:||||:|:|:: ||:||  ::  |:
Db         24 DCPSGWSSYDQHCYRVFKQLKTWDDAERFCSEQAEGGHLVSIESSEEAAFVAQLVPENRR 83

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFE--CFMVSRDTRLREWFKVDCE 113
                |||||||||:| : |        ||:|||| ::      |  : : |   :|  : |
Db         84 RAILYIWIGLRVQGKEKQCSAKWSDGSSVSYENWIEAESKTCLGLQQGTNYHKWVNIYCG 143

Qy        114 QQHSFICK 121
                : : |:|:
Db        144 EINPFVCE 151


RESULT 13
US-09-938-114-2
; Sequence 2, Application US/09938114
; Publication No. US20030022350A1
;   GENERAL INFORMATION:
;        APPLICANT: Chun Wang, Banjamin XY Li, Xin Cheng,
;                   Jing Liu, Li-Wen Niu, Wan-Zhi Huang,
;                   Zhen-Yu Xu, Dan Luo, Lian-Di Kang,
;                   Jin-Guo Ding, Fang Rong, Yan Liu and
;                   Hui-Ran Chen
;        TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE
;                            VENOM OF AGKISTRODON ACUTUS
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: FastSEQ for Windows 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/938,114
;             FILING DATE: 23-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/058,740
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Chen, Anthony C.
;             REGISTRATION NUMBER: 38,673
;             REFERENCE/DOCKET NUMBER: 233/298
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 129 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: Peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-938-114-2

  Query Match             39.1%;  Score 271.5;  DB 10;  Length 129;
  Best Local Similarity   41.4%;  Pred. No. 3.2e-23;
  Matches   53;  Conservative   22;  Mismatches   44;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :| | ||| : :||| ||| || || ||::| ||||:|:|:: || ||  ::    :
Db          1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                 ::||||| ||| : |        |||| || :  :  :|  |  :|   :|    ||
Db         61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120

Qy        114 QQHSFICK 121
                ||  |:|:
Db        121 QQDPFVCE 128


RESULT 14
US-09-929-230-2
; Sequence 2, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
;  APPLICANT: Sheppard, Paul O.
;  APPLICANT:  Bishop, Paul D.
;  TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
;  FILE REFERENCE: 00-72
;  CURRENT APPLICATION NUMBER: US/09/929,230
;  CURRENT FILING DATE:  2001-08-13
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 151
;   TYPE: PRT
;   ORGANISM: Sistrurus miliarius
US-09-929-230-2

  Query Match             26.5%;  Score 184.5;  DB 9;  Length 151;
  Best Local Similarity   32.8%;  Pred. No. 4.5e-13;
  Matches   42;  Conservative   25;  Mismatches   48;  Indels   13;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| |::||| | :  ||  || ||  | :  | |: :: | :||  :     :
Db         20 DCPSDWSSYDQHCYKVFSELKTWDDAESFCYTQHRDSRLASIHSSEEEAFVGKLASQTLK 79

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV-DPFECFMVSRDTRLREWFKVDCEQ 114
              : :  :||||:  :  : |       : : |:     |:   || :  |:  ||   ||:
Db         80 FTS--MWIGLK--DLWKECKWQWSDDTKLDYKAWTRRPYCTVMVVKTDRI-FWFNRGCEK 134

Qy        115 QHSFICKF 122
                ||:|||
Db        135 TVSFVCKF 142
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RESULT 15
US-10-226-420-2
; Sequence 2, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
;  APPLICANT: Sheppard, Paul O.
;  APPLICANT:  Bishop, Paul D.
;  TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
;  FILE REFERENCE: 00-72
;  CURRENT APPLICATION NUMBER: US/10/226,420
;  CURRENT FILING DATE:  2002-08-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 151
;   TYPE: PRT
;   ORGANISM: Sistrurus miliarius
US-10-226-420-2

  Query Match             26.5%;  Score 184.5;  DB 14;  Length 151;
  Best Local Similarity   32.8%;  Pred. No. 4.5e-13;
  Matches   42;  Conservative   25;  Mismatches   48;  Indels   13;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| |::||| | :  ||  || ||  | :   | |: :: | :||  :     :
Db         20 DCPSDWSSYDQHCYKVFSELKTWDDAESFCYTQHRDSRLASIHSSEEEAFVGKLASQTLK 79

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV-DPFECFMVSRDTRLREWFKVDCEQ 114
              : :  :||||:  :  : |       : : |:     |:  || :  |:  ||   ||:
Db         80 FTS--MWIGLK--DLWKECKWQWSDDTKLDYKAWTRRPYCTVMVVKTDRI-FWFNRGCEK 134

Qy        115 QHSFICKF 122
                ||:|||
Db        135 TVSFVCKF 142


RESULT 16
US-09-997-003-30
; Sequence 30, Application US/09997003
; Publication No. US20030203361A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PA003P1
;  CURRENT APPLICATION NUMBER: US/09/997,003
;  CURRENT FILING DATE:  2001-11-30
;  PRIOR APPLICATION NUMBER: unassigned
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: PCT/US00/22157
;  PRIOR FILING DATE: 2000-08-11
;  PRIOR APPLICATION NUMBER: 60/148,680
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-997-003-30

  Query Match             24.2%;  Score 168;  DB 10;  Length 166;
  Best Local Similarity   31.1%;  Pred. No. 4.1e-11;
  Matches   42;  Conservative   25;  Mismatches   50;  Indels   18;  Gaps    5;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || | ::   |||   :   ||  |: :| :    |:|:|| |  | :|| :::   |
Db         34 ISCPEGTNAYRSYCYYFNEDRETWVDADLYC-QNMNSGNLVSVLTQAEGAFVASLI---K 89

Qy         62 EYLTR--YIWIGLRVQNKGQ-----PCSSISYE-------NLVDPFECFMVSRDTRLREW 107
              |  |    :||||    | :       | :||:       : |:|  |  ::  |  ::|
Db         90 ESGTDDFNVWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKW 149

Qy        108 FKVDCEQQHSFICKF 122
                | || : ||:|||
Db        150 KDVPCEDKFSFVCKF 164


RESULT 17
US-09-997-003-43
; Sequence 43, Application US/09997003
; Publication No. US20030203361A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PA003P1
;  CURRENT APPLICATION NUMBER: US/09/997,003
;  CURRENT FILING DATE:  2001-11-30
;  PRIOR APPLICATION NUMBER: unassigned
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: PCT/US00/22157
;  PRIOR FILING DATE: 2000-08-11
;  PRIOR APPLICATION NUMBER: 60/148,680
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-997-003-43

  Query Match             24.2%;  Score 168;  DB 10;  Length 166;
  Best Local Similarity   31.1%;  Pred. No. 4.1e-11;
  Matches   42;  Conservative   25;  Mismatches   50;  Indels   18;  Gaps    5;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || | ::   |||   :   ||  |: :| :    |:|:|| |  | :|| :::   |
Db         34 ISCPEGTNAYRSYCYYFNEDRETWVDADLYC-QNMNSGNLVSVLTQAEGAFVASLI---K 89

Qy         62 EYLTR--YIWIGLRVQNKGQ-----PCSSISYE-------NLVDPFECFMVSRDTRLREW 107
              |  |    :||||    | :       | :||:       : |:|  |  ::  |  ::|
Db         90 ESGTDDFNVWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKW 149

Qy        108 FKVDCEQQHSFICKF 122
                | || : ||:|||
Db        150 KDVPCEDKFSFVCKF 164


RESULT 18
US-10-734-564-2
; Sequence 2, Application US/10734564
; Publication No. US20040157278A1
; GENERAL INFORMATION:
;  APPLICANT: Christopher C Burgess et al
;  TITLE OF INVENTION: Detection Methods Using TIMP1
;  FILE REFERENCE: 1657/2012
;  CURRENT APPLICATION NUMBER: US/10/734,564
;  CURRENT FILING DATE:  2003-12-12
;  NUMBER OF SEQ ID NOS: 138
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-734-564-2

  Query Match             24.2%;  Score 168;  DB 16;  Length 166;
  Best Local Similarity   31.1%;  Pred. No. 4.1e-11;
  Matches   42;  Conservative   25;  Mismatches   50;  Indels   18;  Gaps    5;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || | ::   |||   :   ||  |: :| :    |:|:|| |  | :|| :::   |
Db         34 ISCPEGTNAYRSYCYYFNEDRETWVDADLYC-QNMNSGNLVSVLTQAEGAFVASLI---K 89

Qy         62 EYLTR--YIWIGLRVQNKGQ-----PCSSISYE-------NLVDPFECFMVSRDTRLREW 107
```

```
Db          90 ESGTDDFNVWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKW 149

Qy         108 FKVDCEQQHSFICKF 122
               | || : ||:|||
Db         150 KDVPCEDKFSFVCKF 164


RESULT 19
US-10-734-564-4
; Sequence 4, Application US/10734564
; Publication No. US20040157278A1
; GENERAL INFORMATION:
;  APPLICANT: Christopher C Burgess et al
;  TITLE OF INVENTION: Detection Methods Using TIMP1
;  FILE REFERENCE: 1657/2012
;  CURRENT APPLICATION NUMBER: US/10/734,564
;  CURRENT FILING DATE:  2003-12-12
;  NUMBER OF SEQ ID NOS: 138
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-734-564-4

  Query Match           24.2%;  Score 168;  DB 16;  Length 166;
  Best Local Similarity   31.1%;  Pred. No. 4.1e-11;
  Matches   42;  Conservative   25;  Mismatches   50;  Indels   18;  Gaps    5;

Qy           2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
               : || | ::   |||   :   ||  |: :| :    |:|:|| |  | :|| :::   |
Db          34 ISCPEGTNAYRSYCYYFNEDRETWVDADLYC-QNMNSGNLVSVLTQAEGAFVASLI---K 89

Qy          62 EYLTR--YIWIGLRVQNKGQ-----PCSSISYE-------NLVDPFECFMVSRDTRLREW 107
               |  |    :||||    | :       | :||:       : |:|  |  ::  |  ::|
Db          90 ESGTDDFNVWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKW 149

Qy         108 FKVDCEQQHSFICKF 122
               | || : ||:|||
Db         150 KDVPCEDKFSFVCKF 164


RESULT 20
US-09-925-301-1182
; Sequence 1182, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA106
;  CURRENT APPLICATION NUMBER: US/09/925,301
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05882
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1694
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1182
;   LENGTH: 174
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-301-1182

  Query Match           24.2%;  Score 168;  DB 9;  Length 174;
  Best Local Similarity   31.1%;  Pred. No. 4.4e-11;
  Matches   42;  Conservative   25;  Mismatches   50;  Indels   18;  Gaps    5;

Qy           2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
               : || | ::   |||   :   ||  |: :| :    |:|:|| |  | :|| :::   |
Db          42 ISCPEGTNAYRSYCYYFNEDRETWVDADLYC-QNMNSGNLVSVLTQAEGAFVASLI---K 97

Qy          62 EYLTR--YIWIGLRVQNKGQ-----PCSSISYE-------NLVDPFECFMVSRDTRLREW 107
               |  |    :||||    | :       | :||:       : |:|  |  ::  |  ::|
Db          98 ESGTDDFNVWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKW 157

Qy         108 FKVDCEQQHSFICKF 122
               | || : ||:|||
Db         158 KDVPCEDKFSFVCKF 172


RESULT 21
US-10-028-248A-112
; Sequence 112, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Malyankar, Uriel
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Miller, Charles
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Li, Li
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Colman, Steven
;  APPLICANT:  Tchernev, Velizar
;  APPLICANT:  Si, Jingsheng
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Stone, David
;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Rothenberg, Mark
;  TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods c
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: 21402-222
;  CURRENT APPLICATION NUMBER: US/10/028,248A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/256619
;  PRIOR FILING DATE: 2000-12-19
;  PRIOR APPLICATION NUMBER: 60/262959
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/272408
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/285189
;  PRIOR FILING DATE: 2001-04-20
;  PRIOR APPLICATION NUMBER: 60/308039
;  PRIOR FILING DATE: 2001-07-26
;  PRIOR APPLICATION NUMBER: 60/311266
;  PRIOR FILING DATE: 2001-08-09
;  NUMBER OF SEQ ID NOS: 211
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
;   LENGTH: 175
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-028-248A-112

  Query Match           23.7%;  Score 164.5;  DB 15;  Length 175;
  Best Local Similarity   30.0%;  Pred. No. 1.1e-10;
  Matches   42;  Conservative   20;  Mismatches   57;  Indels   21;  Gaps    4;

Qy           2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDN-VLYAN 60
               : || |  :   |||  |:   ||  ||  | ::  ||||:||  : ||||: : |
Db          38 ISCPKGSQAYGSYCYALFQIPQTWFDAELAC-QKRPGGHLVSVLNSAEASFLSSMVKRTG 96

Qy          61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                    | :| ||||     |  :  :|                    :|   |  :|| :
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Db         97 NSY--QYTWIGLHDPTLGAEPNGGGWEWSNNDVMNYFNWERNPSTALDRAFCGSLSRASG 154

Qy        104 LREWFKVDCEQQHSFICKFT 123
                :|  : || :  ::||||
Db        155 FLKWRDMTCEVKLPYVCKFT 174


RESULT 22
US-10-107-782-112
; Sequence 112, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
;  APPLICANT: Boldog, Ferenc,
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Colman, Steve,
;  APPLICANT:  Edinger, Shlomit,
;  APPLICANT:  Gangolli, Esha,
;  APPLICANT:  Kekuda, Ramesh,
;  APPLICANT:  Li, Li,
;  APPLICANT:  Liu, Xiaohong,
;  APPLICANT:  Malyankar, Uriel,
;  APPLICANT:  Miller, Charles,
;  APPLICANT:  Millet, Isabelle,
;  APPLICANT:  Patturajan, Meera,
;  APPLICANT:  Rothenberg, Mark,
;  APPLICANT:  Sciore, Paul,
;  APPLICANT:  Shenoy, Suresh,
;  APPLICANT:  Shimkets, Richard,
;  APPLICANT:  Si, Jingsheng,
;  APPLICANT:  Smithson, Glennda,
;  APPLICANT:  Spytek, Kimberly,
;  APPLICANT:  Stone, David,
;  APPLICANT:  Taupier, Raymond, jr.,
;  APPLICANT:  Tchernev, Velizar,
;  APPLICANT:  Vernet, Corine,
;  APPLICANT:  Zerhusen, Brian
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
;  FILE REFERENCE: 21402-222CIP
;  CURRENT APPLICATION NUMBER: US/10/107,782
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: 10/028,248
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 60/256,619
;  PRIOR FILING DATE: 2000-12-19
;  PRIOR APPLICATION NUMBER: 60/262,959
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/272,408
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/285,189
;  PRIOR FILING DATE: 2001-04-20
;  PRIOR APPLICATION NUMBER: 60/308,039
;  PRIOR FILING DATE: 2001-07-26
;  PRIOR APPLICATION NUMBER: 60/311,266
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 60/279,344
;  PRIOR FILING DATE: 2001-03-28
;  NUMBER OF SEQ ID NOS: 215
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 112
;   LENGTH: 175
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-107-782-112

  Query Match             23.7%;  Score 164.5;  DB 15;  Length 175;
  Best Local Similarity   30.0%;  Pred. No. 1.1e-10;
  Matches   42;  Conservative   20;  Mismatches   57;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDN-VLYAN 60
              : || |  :   |||  |:   ||  ||  | ::  ||||:||  : ||||: : |
Db         38 ISCPKGSQAYGSYCYALFQIPQTWFDAELAC-QKRPGGHLVSVLNSAEASFLSSMVKRTG 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                |  :| ||||     |  :  :|                    :|   |  :|| :
Db         97 NSY--QYTWIGLHDPTLGAEPNGGGWEWSNNDVMNYFNWERNPSTALDRAFCGSLSRASG 154

Qy        104 LREWFKVDCEQQHSFICKFT 123
                :|  : || :  ::||||
Db        155 FLKWRDMTCEVKLPYVCKFT 174


RESULT 23
US-10-028-248A-111
; Sequence 111, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Malyankar, Uriel
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Miller, Charles
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Li, Li
;  APPLICANT:  Taupier Jr, Raymond J
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Liu, Xiaohong
;  APPLICANT:  Colman, Steven
;  APPLICANT:  Tchernev, Velizar
;  APPLICANT:  Si, Jingsheng
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Stone, David
;  APPLICANT:  Sciore, Paul
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Rothenberg, Mark
;  TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods c
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: 21402-222
;  CURRENT APPLICATION NUMBER: US/10/028,248A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/256619
;  PRIOR FILING DATE: 2000-12-19
;  PRIOR APPLICATION NUMBER: 60/262959
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/272408
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/285189
;  PRIOR FILING DATE: 2001-04-20
;  PRIOR APPLICATION NUMBER: 60/308039
;  PRIOR FILING DATE: 2001-07-26
;  PRIOR APPLICATION NUMBER: 60/311266
;  PRIOR FILING DATE: 2001-08-09
;  NUMBER OF SEQ ID NOS: 211
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
;   LENGTH: 175
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-028-248A-111

  Query Match             22.7%;  Score 157.5;  DB 15;  Length 175;
  Best Local Similarity   30.2%;  Pred. No. 7.2e-10;
  Matches   42;  Conservative   21;  Mismatches   57;  Indels   19;  Gaps    5;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || |  :   |||  |:   ||  ||  | :: : |||:||    ||||: ::: |
Db         38 ISCPKGSQAYGSYCYALFQIPQTWFDAELACQKRPE-GHLVSVLNVAEASFLASMV-KNT 95

Qy         62 EYLTRYIWIGLRVQN-KGQPCSS---------ISYEN-------LVDPFECFMVSRDTRL 104
                :| ||||      |:|             ::| |       :|   |  :|| :
Db         96 GNSYQYTWIGLHDPTLGGEPNGGGWEWSNNDIMNYVNWERNPSTALDRGFCGSLSRSSGF 155
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```
Qy        105 REWFKVDCEQQHSFICKFT 123
                |    || :  ::||||
Db        156 LRWRDTTCEVKLPYVCKFT 174
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RESULT 24
US-10-107-782-111
; Sequence 111, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie
; APPLICANT: Colman, Steve,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gangolli, Esha,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malyankar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glennda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zerhusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10/107,782
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272,408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285,189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308,039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311,266
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/279,344
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 111
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-782-111

Query Match 22.7%; Score 157.5; DB 15; Length 175;
Best Local Similarity 30.2%; Pred. No. 7.2e-10;
Matches 42; Conservative 21; Mismatches 57; Indels 19; Gaps 5;

```
Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || |  :   |||  |:   ||  ||  | :: : |||:||    ||||: :::  |
Db         38 ISCPKGSQAYGSYCYALFQIPQTWFDAELACQKRPE-GHLVSVLNVAEASFLASMV-KNT 95

Qy         62 EYLTRYIWIGLRVQN-KGQPCSS---------ISYEN-------LVDPFECFMVSRDTRL 104
                :| ||||      |:|            ::| |       :|   |  :|| :
Db         96 GNSYQYTWIGLHDPTLGGEPNGGGWEWSNNDIMNYVNWERNPSTALDRGFCGSLSRSSGF 155

Qy        105 REWFKVDCEQQHSFICKFT 123
                |    || :  ::||||
Db        156 LRWRDTTCEVKLPYVCKFT 174
```

RESULT 25
US-10-028-248A-110
; Sequence 110, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Malyankar, Uriel
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gangolli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glennda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchernev, Velizar
; APPLICANT: Si, Jingsheng
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Sciore, Paul
; APPLICANT: Millet, Isabelle
; APPLICANT: Rothenberg, Mark
; TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods c
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 21402-222
; CURRENT APPLICATION NUMBER: US/10/028,248A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-028-248A-110

Query Match 22.2%; Score 154.5; DB 15; Length 175;
Best Local Similarity 30.2%; Pred. No. 1.6e-09;
Matches 42; Conservative 19; Mismatches 59; Indels 19; Gaps 4;

```
Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : ||||  :   :||  ||   ||  |:  | ::   |||:|| :  | ||| : |  |
Db         38 ISCPSGSMAYRSHCYALFKTPKTWMDADIAC-QKRPSGHLVSVLSGAEESFVAS-LVRNN 95

Qy         62 EYLTRYIWIGLRVQNKGQPCSSISYE-------NLV----------DPFECFMVSRDTRL 104
                |||||    :|   ::  :|       | |            |  |  :|| :
Db         96 LNTQSDIWIGLHDPTEGSEANAGGWEWISNDVLNYVAWETDPAAISSPGYCGSLSRSSGY 155
```

```
Qy        105 REWFKVDCEQQHSFICKFT 123
              :|   :|     ::||||
Db        156 LKWRDHNCNLNLPYVCKFT 174
```

RESULT 26
US-10-107-782-110
; Sequence 110, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie
; APPLICANT: Colman, Steve,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gangolli, Esha,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malyankar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glennda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zerhusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10/107,782
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272,408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285,189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308,039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311,266
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/279,344
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 110
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-782-110

Query Match 22.2%; Score 154.5; DB 15; Length 175;
Best Local Similarity 30.2%; Pred. No. 1.6e-09;
Matches 42; Conservative 19; Mismatches 59; Indels 19; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : ||||  :   :||  ||   ||  |:  | ::   |||:|| :  | ||| : |  |
Db         38 ISCPSGSMAYRSHCYALFKTPKTWMDADIAC-QKRPSGHLVSVLSGAEESFVAS-LVRNN 95

Qy         62 EYLTRYIWIGLRVQNKGQPCSSISYE-------NLV----------DPFECFMVSRDTRL 104
                 ||||    :|   ::  :|       | |           |  |  :|| :
Db         96 LNTQSDIWIGLHDPTEGSEANAGGWEWISNDVLNYVAWETDPAAISSPGYCGSLSRSSGY 155
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Qy        105 REWFKVDCEQQHSFICKFT 123
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Db        156 LKWRDHNCNLNLPYVCKFT 174
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RESULT 27
US-10-316-761-3
; Sequence 3, Application US/10316761
; Publication No. US20030109004A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN PANCEATITIS-ASSOCIATED
; PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/316,761
; FILING DATE: 10-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/822,261
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0251 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 262369
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-316-761-3

Query Match 22.1%; Score 153.5; DB 14; Length 175;
Best Local Similarity 25.7%; Pred. No. 2.1e-09;
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :   :||  |    :| .|:  | ::   |:|:|| :  | ||| ::: :
Db         38 IRCPKGSKAYGSHCYALFLSPKSWTDADLAC-QKRPSGNLVSVLSGAEGSFVSSLVKSIG 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE-----------------NLVDPFECFMVSRDTR 103
                |  |:||||    :|   :   :|                    :  |  |  :|| |
Db         97 NSY--SYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYFAWERNPSTISSPGHCASLSRSTA 154

Qy        104 LREWFKVDCEQQHSFICKFT 123
                |   :|  :  ::||||
Db        155 FLRWKDYNCNVRLPYVCKFT 174
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RESULT 28
US-10-434-906-1

; Sequence 1, Application US/10434906
; Publication No. US20030212000A1
; GENERAL INFORMATION:
; APPLICANT: William P. Van Antwerp
; TITLE OF INVENTION: IMMUNOPROTECTIVE METHODS FOR BETA CELL
; TITLE OF INVENTION: NEOGENESIS
; FILE REFERENCE: 130.59-US-U1
; CURRENT APPLICATION NUMBER: US/10/434,906
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 60/379,202
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-434-906-1

Query Match 22.1%; Score 153.5; DB 15; Length 175;
Best Local Similarity 25.7%; Pred. No. 2.1e-09;
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :   :||  |    :|  |:  | ::   |:|:|| :  | ||| ::: :
Db         38 IRCPKGSKAYGSHCYALFLSPKSWTDADLAC-QKRPSGNLVSVLSGAEGSFVSSLVKSIG 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                |   |:||||    :|  :  :|                  :  |  |  :|| |
Db         97 NSY--SYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYFAWERNPSTISSPGHCASLSRSTA 154

Qy        104 LREWFKVDCEQQHSFICKFT 123
                |   :|  :  ::||||
Db        155 FLRWKDYNCNVRLPYVCKFT 174
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RESULT 29
US-10-028-248A-109
; Sequence 109, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Malyankar, Uriel
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gangolli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glennda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchernev, Velizar
; APPLICANT: Si, Jingsheng
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Sciore, Paul
; APPLICANT: Millet, Isabelle
; APPLICANT: Rothenberg, Mark
; TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 21402-222
; CURRENT APPLICATION NUMBER: US/10/028,248A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-028-248A-109

Query Match 22.1%; Score 153.5; DB 15; Length 175;
Best Local Similarity 25.7%; Pred. No. 2.1e-09;
Matches 36; Conservative 24; Mismatches 59; Indels 21; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :   :||  |    :|  |:  | ::   |:|:|| :  | ||| ::: :
Db         38 IRCPKGSKAYGSHCYALFLSPKSWTDADLAC-QKRPSGNLVSVLSGAEGSFVSSLVKSIG 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                |   |:||||    :|  :  :|                  :  |  |  :|| |
Db         97 NSY--SYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYFAWERNPSTISSPGHCASLSRSTA 154

Qy        104 LREWFKVDCEQQHSFICKFT 123
                |   :|  :  ::||||
Db        155 FLRWKDYNCNVRLPYVCKFT 174
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RESULT 30
US-10-107-782-109
; Sequence 109, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie
; APPLICANT: Colman, Steve,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gangolli, Esha,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malyankar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glennda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Taupier, Raymond, jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zerhusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10/107,782
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19

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;  PRIOR APPLICATION NUMBER: 60/272,408
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: 60/285,189
;  PRIOR FILING DATE: 2001-04-20
;  PRIOR APPLICATION NUMBER: 60/308,039
;  PRIOR FILING DATE: 2001-07-26
;  PRIOR APPLICATION NUMBER: 60/311,266
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 60/279,344
;  PRIOR FILING DATE: 2001-03-28
;  NUMBER OF SEQ ID NOS: 215
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 109
;   LENGTH: 175
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-107-782-109

  Query Match             22.1%;  Score 153.5;  DB 15;  Length 175;
  Best Local Similarity   25.7%;  Pred. No. 2.1e-09;
  Matches   36;  Conservative   24;  Mismatches   59;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :   :||  |    :|  |:  | ::   |:|:|| : . | ||| ::: :
Db         38 IRCPKGSKAYGSHCYALFLSPKSWTDADLAC-QKRPSGNLVSVLSGAEGSFVSSLVKSIG 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE-----------------NLVDPFECFMVSRDTR 103
                 |   |:||||    :|   :  :|                 :  |  |  :|| |
Db         97 NSY--SYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYFAWERNPSTISSPGHCASLSRSTA 154

Qy        104 LREWFKVDCEQQHSFICKFT 123
                |   :|  :  ::||||
Db        155 FLRWKDYNCNVRLPYVCKFT 174


RESULT 31
US-09-925-301-1013
; Sequence 1013, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA106
;  CURRENT APPLICATION NUMBER: US/09/925,301
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05882
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1694
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1013
;   LENGTH: 183
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-301-1013

  Query Match             22.1%;  Score 153.5;  DB 9;  Length 183;
  Best Local Similarity   25.7%;  Pred. No. 2.2e-09;
  Matches   36;  Conservative   24;  Mismatches   59;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :   :||  |    :|  |:  | ::  .|:|:|| :  | ||| ::: :
Db         46 IRCPKGSKAYGSHCYALFLSPKSWTDADLAC-QKRPSGNLVSVLSGAEGSFVSSLVKSIG 104

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE-----------------NLVDPFECFMVSRDTR 103
                 |   |:||||    :|   :  :|                 :  |  |  :|| |
Db        105 NSY--SYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYFAWERNPSTISSPGHCASLSRSTA 162

Qy        104 LREWFKVDCEQQHSFICKFT 123
                |   :|  :  ::||||
Db        163 FLRWKDYNCNVRLPYVCKFT 182


RESULT 32
US-09-978-295A-452
; Sequence 452, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C11
;  CURRENT APPLICATION NUMBER: US/09/978,295A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/064249
;  PRIOR FILING DATE: 1997-11-03
;  PRIOR APPLICATION NUMBER: 60/065311
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: 60/066364
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: 60/077450
;  PRIOR FILING DATE: 1998-03-10
;  PRIOR APPLICATION NUMBER: 60/077632
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077641
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077649
;  PRIOR FILING DATE: 1998-03-11
;  PRIOR APPLICATION NUMBER: 60/077791
;  PRIOR FILING DATE: 1998-03-12
;  PRIOR APPLICATION NUMBER: 60/078004
;  PRIOR FILING DATE: 1998-03-13
;  PRIOR APPLICATION NUMBER: 60/078886
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078936
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078910
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/078939
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/079294
;  PRIOR FILING DATE: 1998-03-25
;  PRIOR APPLICATION NUMBER: 60/079656
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: 60/079664
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 9; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
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Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
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Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

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Db        155 FLKWKDYNCDAKLPYVCKF 173
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RESULT 33
US-09-978-697-452
; Sequence 452, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 9; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
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Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

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Db 155 FLKWKDYNCDAKLPYVCKF 173

RESULT 34
US-09-978-192A-452
; Sequence 452, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-05-15
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Query Match 21.4%; Score 148.5; DB 9; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
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Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
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RESULT 35
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; Sequence 452, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
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;  APPLICANT:  Wood, William I.
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;  TITLE OF INVENTION:  Acids Encoding the Same
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;  PRIOR APPLICATION NUMBER: 60/080165
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;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/080327
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;  PRIOR APPLICATION NUMBER: 60/081955
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;  PRIOR FILING DATE: 1998-04-22
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;  PRIOR FILING DATE: 1998-04-27
;  PRIOR APPLICATION NUMBER: 60/083322
;  PRIOR FILING DATE: 1998-04-28
;  PRIOR APPLICATION NUMBER: 60/083392
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; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
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; PRIOR APPLICATION NUMBER: 60/084640
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 9; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :    ||  |    :|  |:  | ::   | |:|| :  | ||| ::: : :
Db         38 ISCPKGSKAYGSPCYALFLSPKSWMDADLAC-QKRPSGKLVSVLSGAEGSFVSSLVRSIS 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                |   ||||||    :|       :|                    :::|  |  :|| |
Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

Qy        104 LREWFKVDCEQQHSFICKF 122
                :|   :|: :  .::|||
Db        155 FLKWKDYNCDAKLPYVCKF 173
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RESULT 36
US-09-978-189-452
; Sequence 452, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-03-25
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
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Db         38 ISCPKGSKAYGSPCYALFLSPKSWMDADLAC-QKRPSGKLVSVLSGAEGSFVSSLVRSIS 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
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Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154
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Qy        104 LREWFKVDCEQQHSFICKF 122
                :|   :|: :  ::|||
Db        155 FLKWKDYNCDAKLPYVCKF 173


RESULT 37
US-09-978-608A-452
; Sequence 452, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C22
;  CURRENT APPLICATION NUMBER: US/09/978,608A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 452
;   LENGTH: 175
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-978-608A-452

  Query Match             21.4%;  Score 148.5;  DB 10;  Length 175;
  Best Local Similarity   25.9%;  Pred. No. 8e-09;
  Matches   36;  Conservative   25;  Mismatches   57;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
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Db         38 ISCPKGSKAYGSPCYALFLSPKSWMDADLAC-QKRPSGKLVSVLSGAEGSFVSSLVRSIS 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                |   ||||||    :|       :|                  :::|  |  :|| |
Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

Qy        104 LREWFKVDCEQQHSFICKF 122
                :|   :|: :  ::|||
Db        155 FLKWKDYNCDAKLPYVCKF 173


RESULT 38
US-09-978-585A-452
; Sequence 452, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C15
;  CURRENT APPLICATION NUMBER: US/09/978,585A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 452
;   LENGTH: 175
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-978-585A-452

  Query Match             21.4%;  Score 148.5;  DB 10;  Length 175;
  Best Local Similarity   25.9%;  Pred. No. 8e-09;
  Matches   36;  Conservative   25;  Mismatches   57;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :    ||  |    :|  |:  | ::   | |:|| :  | ||| ::: : :
Db         38 ISCPKGSKAYGSPCYALFLSPKSWMDADLAC-QKRPSGKLVSVLSGAEGSFVSSLVRSIS 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                |   ||||||    :|       :|                  :::|  |  :|| |
Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

Qy        104 LREWFKVDCEQQHSFICKF 122
                :|   :|: :  ::|||
Db        155 FLKWKDYNCDAKLPYVCKF 173


RESULT 39
US-09-978-191A-452
; Sequence 452, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
```

; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
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; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
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Query Match 21.4%; Score 148.5; DB 10; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
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Query Match 21.4%; Score 148.5; DB 10; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
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Db         38 ISCPKGSKAYGSPCYALFLSPKSWMDADLAC-QKRPSGKLVSVLSGAEGSFVSSLVRSIS 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
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Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

Qy        104 LREWFKVDCEQQHSFICKF 122
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Db        155 FLKWKDYNCDAKLPYVCKF 173
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RESULT 42
US-09-999-833A-452
; Sequence 452, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
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Db         38 ISCPKGSKAYGSPCYALFLSPKSWMDADLAC-QKRPSGKLVSVLSGAEGSFVSSLVRSIS 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                |  ||||||    :|       :|                   :::|  |  :|| |
Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

Qy        104 LREWFKVDCEQQHSFICKF 122
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Db        155 FLKWKDYNCDAKLPYVCKF 173
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RESULT 43
US-09-981-915A-452
; Sequence 452, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

```
Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
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Db         38 ISCPKGSKAYGSPCYALFLSPKSWMDADLAC-QKRPSGKLVSVLSGAEGSFVSSLVRSIS 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                 |   ||||||    :|       :|                :::|  |  :|| |
Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

Qy        104 LREWFKVDCEQQHSFICKF 122
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Db        155 FLKWKDYNCDAKLPYVCKF 173
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RESULT 44
US-09-978-824-452
; Sequence 452, Application US/09978824
; Publication No. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-03-27
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; PRIOR APPLICATION NUMBER: 60/080327
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
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Db         38 ISCPKGSKAYGSPCYALFLSPKSWMDADLAC-QKRPSGKLVSVLSGAEGSFVSSLVRSIS 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
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Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

Qy        104 LREWFKVDCEQQHSFICKF 122
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Db        155 FLKWKDYNCDAKLPYVCKF 173
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RESULT 45
US-09-918-585A-452
; Sequence 452, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C1
; CURRENT APPLICATION NUMBER: US/09/918,585A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/086023

Query Match 21.4%; Score 148.5; DB 10; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
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Db         38 ISCPKGSKAYGSPCYALFLSPKSWMDADLAC-QKRPSGKLVSVLSGAEGSFVSSLVRSIS 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
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Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

Qy        104 LREWFKVDCEQQHSFICKF 122
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Db        155 FLKWKDYNCDAKLPYVCKF 173
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RESULT 46
US-09-999-834A-452
; Sequence 452, Application US/09999834A
; Publication No. US20030064407A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C75
; CURRENT APPLICATION NUMBER: US/09/999,834A
; CURRENT FILING DATE: 2001-10-24
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

```
Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
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Db         38 ISCPKGSKAYGSPCYALFLSPKSWMDADLAC-QKRPSGKLVSVLSGAEGSFVSSLVRSIS 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
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Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

Qy        104 LREWFKVDCEQQHSFICKF 122
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Db        155 FLKWKDYNCDAKLPYVCKF 173
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RESULT 47
US-09-978-423A-452
; Sequence 452, Application US/09978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C21
; CURRENT APPLICATION NUMBER: US/09/978,423A
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
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Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

Qy        104 LREWFKVDCEQQHSFICKF 122
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Db        155 FLKWKDYNCDAKLPYVCKF 173
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RESULT 48
US-09-978-193A-452
; Sequence 452, Application US/09978193A
; Publication No. US20030073624A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C6
; CURRENT APPLICATION NUMBER: US/09/978,193A
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 21.4%; Score 148.5; DB 10; Length 175;
Best Local Similarity 25.9%; Pred. No. 8e-09;
Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
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Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
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Db         97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

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Db        155 FLKWKDYNCDAKLPYVCKF 173
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RESULT 49
US-09-999-830A-452
; Sequence 452, Application US/09999830A
; Publication No. US20030077700A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 21.4%; Score 148.5; DB 10; Length 175;
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Matches 36; Conservative 25; Mismatches 57; Indels 21; Gaps 4;

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C26
; CURRENT APPLICATION NUMBER: US/09/978,757A
; CURRENT FILING DATE: 2002-03-19
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Job time : 58 secs

OM protein - protein search, using sw model

Run on: May 2, 2005, 15:59:07 ; Search time 24 Seconds
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Post-processing: Minimum Match 0%
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Listing first 65 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	661	95.1	127	1	US-07-614-443A-1	Sequence 1, Appli
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ALIGNMENTS

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; Patent No. 6710031
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOYUKI
; APPLICANT: KITO, MORIKAZU
; APPLICANT: KAYAHARA, TAKASHI
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHKI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING TH
; FILE REFERENCE: 214760US0
; CURRENT APPLICATION NUMBER: US/09/969,763
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; ORGANISM: Crotallus horridus
US-09-969-763-1

Query Match 100.0%; Score 695; DB 4; Length 126;
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;    APPLICANT:  FUKUCHI, Naoyuki
;    APPLICANT:  YAMAMOTO, Hiroshi
;    APPLICANT:  NAGANO, Mitsuyo
;    APPLICANT:  KITO, Morikazu
;    APPLICANT:  TANAKA, Akiko
;    APPLICANT:  ISHII, Koichi
;    APPLICANT:  KOBAYASHI, Tsuyoshi
;    APPLICANT:  YOSHIMOTO, Ryota
;    TITLE OF INVENTION:  PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
;    TITLE OF INVENTION:  METHOD OF PRODUCING THE SAME
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,840A
;      FILING DATE:  20-MAR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-236975
;      FILING DATE:  22-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5856126man F. Oblon
;      REGISTRATION NUMBER:  24,618
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-612-840A-2

  Query Match             98.4%;  Score 684;  DB 2;  Length 126;
  Best Local Similarity   98.4%;  Pred. No. 1.8e-76;
  Matches  124;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 3
US-08-612-840A-8
; Sequence 8, Application US/08612840A
; Patent No. 5856126
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUCHI, Naoyuki
;    APPLICANT:  YAMAMOTO, Hiroshi
;    APPLICANT:  NAGANO, Mitsuyo
;    APPLICANT:  KITO, Morikazu
;    APPLICANT:  TANAKA, Akiko
;    APPLICANT:  ISHII, Koichi
;    APPLICANT:  KOBAYASHI, Tsuyoshi
;    APPLICANT:  YOSHIMOTO, Ryota
;    TITLE OF INVENTION:  PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
;    TITLE OF INVENTION:  METHOD OF PRODUCING THE SAME
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,840A
;      FILING DATE:  20-MAR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-236975
;      FILING DATE:  22-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5856126man F. Oblon
;      REGISTRATION NUMBER:  24,618
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  149 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-612-840A-8

  Query Match             98.4%;  Score 684;  DB 2;  Length 149;
  Best Local Similarity   98.4%;  Pred. No. 2.2e-76;
  Matches  124;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         24 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 143

Qy        121 KFTRPR 126
              ||||||
Db        144 KFTRPR 149
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RESULT 4
US-09-969-763-3
; Sequence 3, Application US/09969763
; Patent No. 6710031
; GENERAL INFORMATION:
;  APPLICANT: FUKUCHI, NAOYUKI
;  APPLICANT:  KITO, MORIKAZU
;  APPLICANT:  KAYAHARA, TAKASHI
;  APPLICANT:  FUTAKI, FUMIE
;  APPLICANT:  ISHIKAWA, KOHKI
;  APPLICANT:  SUZUKI, EIICHIRO
;  APPLICANT:  GONDOH, KEIKO
;  APPLICANT:  SHIMBA, NOBUHISA
;  APPLICANT:  YAMADA, NAOYUKI
;  TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING T
;  FILE REFERENCE: 214760US0
;  CURRENT APPLICATION NUMBER: US/09/969,763
;  CURRENT FILING DATE:  2000-10-25
;  PRIOR APPLICATION NUMBER: JP 2000-305279
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Crotalus harridus
US-09-969-763-3

  Query Match             98.4%;  Score 684;  DB 4;  Length 149;
  Best Local Similarity   98.4%;  Pred. No. 2.2e-76;
  Matches  124;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              ||||||||| ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         24 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 83

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 143

Qy        121 KFTRPR 126
              ||||||
Db        144 KFTRPR 149


RESULT 5
US-07-614-443A-1
; Sequence 1, Application US/07614443A
; Patent No. 5342830
;  GENERAL INFORMATION:
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  ANTITHROMBOSIS AGENTS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/614,443A
;      FILING DATE:  19901116
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22803-20003.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  127 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-614-443A-1

  Query Match             95.1%;  Score 661;  DB 1;  Length 127;
  Best Local Similarity   96.0%;  Pred. No. 1.2e-73;
  Matches  121;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              ||||||||| ||||||||||||||| |||||||||| ||||||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGRHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSIYSENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 6
US-08-294-859-1
; Sequence 1, Application US/08294859
; Patent No. 5679542
;  GENERAL INFORMATION:
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  ANTITHROMBOSIS AGENTS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/294,859
;      FILING DATE:  29-AUG-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2803-0003.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  127 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-294-859-1

  Query Match             95.1%;  Score 661;  DB 1;  Length 127;
  Best Local Similarity   96.0%;  Pred. No. 1.2e-73;
  Matches  121;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
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Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||||| |||||||||| ||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGRHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSIYSENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 7
US-08-481-676-1
; Sequence 1, Application US/08481676
; Patent No. 5744584
;  GENERAL INFORMATION:
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  ANTITHROMBOSIS AGENTS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,676
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/294,859
;      FILING DATE:  29-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2803-0003.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  127 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-481-676-1

  Query Match             95.1%;  Score 661;  DB 1;  Length 127;
  Best Local Similarity   96.0%;  Pred. No. 1.2e-73;
  Matches  121;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| ||||||||||||||| |||||||||| ||||||||||||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKGRHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRVQNKGQPCSSIYSENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120

Qy        121 KFTRPR 126
              ||||||
Db        121 KFTRPR 126


RESULT 8
US-09-969-763-10
; Sequence 10, Application US/09969763
; Patent No. 6710031
; GENERAL INFORMATION:
;  APPLICANT: FUKUCHI, NAOYUKI
;  APPLICANT:  KITO, MORIKAZU
;  APPLICANT:  KAYAHARA, TAKASHI
;  APPLICANT:  FUTAKI, FUMIE
;  APPLICANT:  ISHIKAWA, KOHKI
;  APPLICANT:  SUZUKI, EIICHIRO
;  APPLICANT:  GONDOH, KEIKO
;  APPLICANT:  SHIMBA, NOBUHISA
;  APPLICANT:  YAMADA, NAOYUKI
;  TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING TH
;  FILE REFERENCE: 214760US0
;  CURRENT APPLICATION NUMBER: US/09/969,763
;  CURRENT FILING DATE:  2000-10-25
;  PRIOR APPLICATION NUMBER: JP 2000-305279
;  PRIOR FILING DATE: 2000-10-04
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-969-763-10

  Query Match             78.0%;  Score 542;  DB 4;  Length 110;
  Best Local Similarity   81.7%;  Pred. No. 4.8e-59;
  Matches  103;  Conservative    1;  Mismatches    6;  Indels   16;  Gaps    1;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |||||||||| |||||||||||:| ||||||||||||||||||||||||||||||||||
Db          1 DLECPSGWSSYSRYCYKPFKQEMTYADAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              |||||||||||||                  ||||||||||||||||||||||||||||
Db         61 KEYLTRYIWIGLRFFF---------------FECFMVSRDTRLREWFKVDCEQQHSFIC 104

Qy        121 KFTRPR 126
              ||||||
Db        105 KFTRPR 110


RESULT 9
US-07-893-929A-7
; Sequence 7, Application US/07893929A
; Patent No. 5336667
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/893,929A
;      FILING DATE:  19920605
```

```
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/803,630
;       FILING DATE:  December 3, 1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Monaco, Daniel A.
;       REGISTRATION NUMBER:  30,480
;       REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 568-8383
;       TELEFAX:  (215) 568-5549
;       TELEX:  No. 5336667e
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  130 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  linear
US-07-893-929A-7

  Query Match             49.0%;  Score 340.5;  DB 1;  Length 130;
  Best Local Similarity   50.8%;  Pred. No. 4.2e-34;
  Matches   66;  Conservative   22;  Mismatches   29;  Indels   13;  Gaps    4;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN-K 61
              :||| |||  :|||:  |:  ||  |||||||||  |||:|:|:  || ||  :|  | |
Db          1 DCPSDWSSFKQYCYQIVKELKTWEDAERFCSEQANDGHLVSIESYREAVFVAELLSENVK 60

Qy         62 EYLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDC 112
              :|   ::|||| |||||| |        ||:||||||  :| :||:: :::  : |  | |
Db         61 KY---HVWIGLSVQNKGQQCSSEWSDGSSVSYENLVKPNPKKCFVLKKESEFKTWSNVYC 117

Qy        113 EQQHSFICKF 122
              ||:| |:|||
Db        118 EQKHIFMCKF 127


RESULT 10
PCT-US92-10344-7
; Sequence 7, Application PC/TUS9210344
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10344
;      FILING DATE:  19921201
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  130 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
PCT-US92-10344-7

  Query Match             49.0%;  Score 340.5;  DB 5;  Length 130;
  Best Local Similarity   50.8%;  Pred. No. 4.2e-34;
  Matches   66;  Conservative   22;  Mismatches   29;  Indels   13;  Gaps    4;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN-K 61
              :||| |||  :|||:  |:  ||  |||||||||  |||:|:|:  || ||  :|  | |
Db          1 DCPSDWSSFKQYCYQIVKELKTWEDAERFCSEQANDGHLVSIESYREAVFVAELLSENVK 60

Qy         62 EYLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDC 112
              :|   ::|||| |||||| |        ||:||||||  :| :||:: :::  : |  | |
Db         61 KY---HVWIGLSVQNKGQQCSSEWSDGSSVSYENLVKPNPKKCFVLKKESEFKTWSNVYC 117

Qy        113 EQQHSFICKF 122
              ||:| |:|||
Db        118 EQKHIFMCKF 127


RESULT 11
US-07-893-929A-1
; Sequence 1, Application US/07893929A
; Patent No. 5336667
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/893,929A
;      FILING DATE:  19920605
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  No. 5336667e
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  131 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-893-929A-1

  Query Match             47.0%;  Score 326.5;  DB 1;  Length 131;
  Best Local Similarity   46.6%;  Pred. No. 2.3e-32;
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  Matches   61;  Conservative   20;  Mismatches   41;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| |:|||: ||:  ||  |||||||||  |||:|:|:| || ||  ::  |
Db          1 DCPSDWSSYDQYCYRVFKRLQTWEDAERFCSEQANDGHLVSIESAGEADFVTQLVSENIR 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVD--PFECFMVSRDTRLREWFKVDCE 113
                |:||||||| ||| |        ||: |:|| :    :|: : :    | |  | |
Db         61 SEKHYVWIGLRVQGKGQQCSSEWSDGSSVHYDNLQEKNTRKCYGLEKRAEFRTWSNVYCG 120

Qy        114 QQHSFICKFTR 124
              ::  |:||| |
Db        121 HEYPFVCKFXR 131


RESULT 12
PCT-US92-10344-1
; Sequence 1, Application PC/TUS9210344
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10344
;      FILING DATE:  19921201
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  131 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
PCT-US92-10344-1

  Query Match             47.0%;  Score 326.5;  DB 5;  Length 131;
  Best Local Similarity   46.6%;  Pred. No. 2.3e-32;
  Matches   61;  Conservative   20;  Mismatches   41;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| |:|||: ||:  ||  |||||||||  |||:|:|:| || ||  ::  |
Db          1 DCPSDWSSYDQYCYRVFKRLQTWEDAERFCSEQANDGHLVSIESAGEADFVTQLVSENIR 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVD--PFECFMVSRDTRLREWFKVDCE 113
                |:||||||| ||| |        ||: |:|| :    :|: : :    | |  | |
Db         61 SEKHYVWIGLRVQGKGQQCSSEWSDGSSVHYDNLQEKNTRKCYGLEKRAEFRTWSNVYCG 120

Qy        114 QQHSFICKFTR 124
              ::  |:||| |
Db        121 HEYPFVCKFXR 131


RESULT 13
US-07-893-929A-5
; Sequence 5, Application US/07893929A
; Patent No. 5336667
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/893,929A
;      FILING DATE:  19920605
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  No. 5336667e
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  132 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-893-929A-5

  Query Match             46.8%;  Score 325.5;  DB 1;  Length 132;
  Best Local Similarity   47.3%;  Pred. No. 3e-32;
  Matches   61;  Conservative   22;  Mismatches   37;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| |||  :|||:  |:  ||  ||:||||||  |||:|:|:  || ||  :|  | :
Db          1 DCPSDWSSFKQYCYQIVKELKTWEDAEKFCSEQANDGHLVSIESYREAVFVAELLSENVK 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                :|||| |||| | |        ||: ||||:  :| :||:: :::  | |  | ||
Db         61 TTKYNVWIGLSVQNKEQQCSSEWSDGSSVXYENLIKPNPKKCFVLKKESEFRTWSNVYCE 120

Qy        114 QQHSFICKF 122
              |:| |:|||
Db        121 QKHIFMCKF 129


RESULT 14
PCT-US92-10344-5
; Sequence 5, Application PC/TUS9210344
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
```

```
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10344
;      FILING DATE:  19921201
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  132 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
PCT-US92-10344-5

  Query Match             46.8%;  Score 325.5;  DB 5;  Length 132;
  Best Local Similarity   47.3%;  Pred. No. 3e-32;
  Matches   61;  Conservative   22;  Mismatches   37;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| |||  :|||:  |:  ||  ||:||||||  |||:|:|:  || ||  :|  | :
Db          1 DCPSDWSSFKQYCYQIVKELKTWEDAEKFCSEQANDGHLVSIESYREAVFVAELLSENVK 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                 :|||| |||| | |        ||: ||||:  :| :||:: :::  | |  | ||
Db         61 TTKYNVWIGLSVQNKEQQCSSEWSDGSSVXYENLIKPNPKKCFVLKKESEFRTWSNVYCE 120

Qy        114 QQHSFICKF 122
                |:| |:|||
Db        121 QKHIFMCKF 129


RESULT 15
US-07-893-929A-2
; Sequence 2, Application US/07893929A
; Patent No. 5336667
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/893,929A
;      FILING DATE:  19920605
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  No. 5336667e
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  134 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-893-929A-2

  Query Match             44.2%;  Score 307.5;  DB 1;  Length 134;
  Best Local Similarity   42.0%;  Pred. No. 5.1e-30;
  Matches   55;  Conservative   26;  Mismatches   41;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  |  |||: |:|||: | :   |  |||||::||  |||:|:||  || ||  ::  |
Db          1 DFHCLPGWSAYDQYCYRVFNEPKNWEDAERFCAKQADSGHLVSIETMGEADFVAQLISEN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
                :    |:||||:|||| | |       ||::||||:  :  :|  : :::  |:|  :
Db         61 IQSKEHYVWIGLKVQNKEQQCSSEWSDGSSVTYENLIKLYMRKCGALEQESGFRKWINLG 120

Qy        112 CEQQHSFICKF 122
              | | : |:|||
Db        121 CIQLNPFVCKF 131


RESULT 16
PCT-US92-10344-2
; Sequence 2, Application PC/TUS9210344
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10344
;      FILING DATE:  19921201
;      CLASSIFICATION:
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  134 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
PCT-US92-10344-2

  Query Match             44.2%;  Score 307.5;  DB 5;  Length 134;
  Best Local Similarity   42.0%;  Pred. No. 5.1e-30;
  Matches   55;  Conservative   26;  Mismatches   41;  Indels    9;  Gaps    2;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              |  |. |||: |:|||: | :   |  |||||::||  |||:|:||  || ||  ::  |
Db          1 DFHCLPGWSAYDQYCYRVFNEPKNWEDAERFCAKQADSGHLVSIETMGEADFVAQLISEN 60

Qy         61 KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPF--ECFMVSRDTRLREWFKVD 111
               :    |:||||:|||| | |       ||::||||:  :  :|  : :::  |:|  :
Db         61 IQSKEHYVWIGLKVQNKEQQCSSEWSDGSSVTYENLIKLYMRKCGALEQESGFRKWINLG 120

Qy        112 CEQQHSFICKF 122
              | | : |:|||
Db        121 CIQLNPFVCKF 131


RESULT 17
US-09-058-740-2
; Sequence 2, Application US/09058740
; Patent No. 6489451
;  GENERAL INFORMATION:
;       APPLICANT: Chun Wang, Banjamin XY Li, Xin Cheng,
;                  Jing Liu, Li-Wen Niu, Wan-Zhi Huang,
;                  Zhen-Yu Xu, Dan Luo, Lian-Di Kang,
;                  Jin-Guo Ding, Fang Rong, Yan Liu and
;                  Hui-Ran Chen
;       TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE
;                           VENOM OF AGKISTRODON ACUTUS
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Lyon & Lyon
;            STREET: 633 West Fifth Street
;                    Suite 4700
;            CITY: Los Angeles
;            STATE: California
;            COUNTRY: U.S.A.
;            ZIP: 90071-2066
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                         storage
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: IBM P.C. DOS 5.0
;            SOFTWARE: FastSEQ for Windows 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/058,740
;            FILING DATE: 10-Apr-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: <Unknown>
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Chen, Anthony C.
;            REGISTRATION NUMBER: 38,673
;            REFERENCE/DOCKET NUMBER: 233/298
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (213) 489-1600
;            TELEFAX: (213) 955-0440
;            TELEX: 67-3510
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 129 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: Peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-058-740-2

  Query Match             39.1%;  Score 271.5;  DB 4;  Length 129;
  Best Local Similarity   41.4%;  Pred. No. 1.3e-25;
  Matches   53;  Conservative   22;  Mismatches   44;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :| | ||| : :||| |||  ||  || ||::|  ||||:|:|:: || ||  ::    :
Db          1 DCSSDWSSYEGHCYKVFKQSKTWTDAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIK 60

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLV--DPFECFMVSRDTRLREWFKVDCE 113
                 ::||||| ||| : |       |||| || :  :  :|  |  :|   :|    ||
Db         61 SAKIHVWIGLRAQNKEKQCSIEWSDGSSISKENWIEEESKKCLGVHIETGFHKWENFYCE 120

Qy        114 QQHSFICK 121
              ||  |:|:
Db        121 QQDPFVCE 128


RESULT 18
US-07-893-929A-9
; Sequence 9, Application US/07893929A
; Patent No. 5336667
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/893,929A
;      FILING DATE:  19920605
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  No. 5336667e
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  133 amino acids
```

```
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-893-929A-9

  Query Match             36.9%;  Score 256.5;  DB 1;  Length 133;
  Best Local Similarity   37.8%;  Pred. No. 9.8e-24;
  Matches   51;  Conservative   30;  Mismatches   43;  Indels   11;  Gaps    4;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :| ||||  : :||: |: : ||  ||::|: |  ||||:|:|:  :| ||  ::
Db          1 DQDCLSGWSFYEGHCYQLFRLK-TWDEAEKYCN-QWDGGHLVSIESNAKAEFVAQLISRK 58

Qy         61 --KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKVD 111
                |  :   :||||| ::| : |       | : ||::| | :||:: | |  |:|  |:
Db         59 LPKSAIEDRVWIGLRDRSKREQCGHLWTDNSFVHYEHVVPPTKCFVLERQTEFRKWIAVN 118

Qy        112 CEQQHSFICKFTRPR 126
              || :  |:||   ||
Db        119 CEFKFPPFVCKAKIPR 133


RESULT 19
PCT-US92-10344-9
; Sequence 9, Application PC/TUS9210344
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10344
;      FILING DATE:  19921201
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  133 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
PCT-US92-10344-9

  Query Match             36.9%;  Score 256.5;  DB 5;  Length 133;
  Best Local Similarity   37.8%;  Pred. No. 9.8e-24;
  Matches   51;  Conservative   30;  Mismatches   43;  Indels   11;  Gaps    4;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYAN 60
              | :| ||||  : :||: |: : ||  ||::|: |  ||||:|:|:  :| ||  ::
Db          1 DQDCLSGWSFYEGHCYQLFRLK-TWDEAEKYCN-QWDGGHLVSIESNAKAEFVAQLISRK 58

Qy         61 --KEYLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKVD 111
                |  :   :||||| ::| : |       | : ||::| | :||:: | |  |:|  |:
Db         59 LPKSAIEDRVWIGLRDRSKREQCGHLWTDNSFVHYEHVVPPTKCFVLERQTEFRKWIAVN 118

Qy        112 CEQQHSFICKFTRPR 126
              || :  |:||   ||
Db        119 CEFKFPPFVCKAKIPR 133


RESULT 20
US-07-893-929A-4
; Sequence 4, Application US/07893929A
; Patent No. 5336667
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/893,929A
;      FILING DATE:  19920605
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  No. 5336667e
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-893-929A-4

  Query Match             36.2%;  Score 251.5;  DB 1;  Length 123;
  Best Local Similarity   39.7%;  Pred. No. 3.7e-23;
  Matches   52;  Conservative   22;  Mismatches   36;  Indels   21;  Gaps    6;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDN----VLY 58
              :||| ||| : :||: | :   || ||:||::| || ||:| ::: || ||      :|
Db          1 DCPSDWSSYEGHCYRVFNEPQNWADAEKFCTQQHKGSHLVSFQSSEEADFVVQMTRPILN 60

Qy         59 ANKEYLTRYIWIGLRVQNKGQPCSS-------ISYENLVDPFECFMVSRDTRLREWFKVD 111
              ||       :||||    |    |:|       : |:   : ||| :||| |   ||  :|
Db         61 AN------LVWIGL--SNLWNGCNSQWSDGTXLDYKXWREQFEC-LVSRTTN-NEWLSMD 110

Qy        112 CEQQHSFICKF 122
              |   |||:|:|
Db        111 CSSTHSFVCEF 121
```

```
RESULT 21
PCT-US92-10344-4
; Sequence 4, Application PC/TUS9210344
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10344
;      FILING DATE:  19921201
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
PCT-US92-10344-4

  Query Match             36.2%;  Score 251.5;  DB 5;  Length 123;
  Best Local Similarity   39.7%;  Pred. No. 3.7e-23;
  Matches   52;  Conservative   22;  Mismatches   36;  Indels   21;  Gaps    6;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDN----VLY 58
              :||| ||| : :||: | :   || ||:||::| || ||:| ::: || ||      :|
Db          1 DCPSDWSSYEGHCYRVFNEPQNWADAEKFCTQQHKGSHLVSFQSSEEADFVVQMTRPILN 60

Qy         59 ANKEYLTRYIWIGLRVQNKGQPCSS-------ISYENLVDPFECFMVSRDTRLREWFKVD 111
              ||       :|||| |    |:|       : |:   : ||| :||| |   ||  :|
Db         61 AN------LVWIGL--SNLWNGCNSQWSDGTXLDYKXWREQFEC-LVSRTTN-NEWLSMD 110

Qy        112 CEQQHSFICKF 122
              |   |||:|:|
Db        111 CSSTHSFVCEF 121


RESULT 22
US-07-614-443A-2
; Sequence 2, Application US/07614443A
; Patent No. 5342830
;  GENERAL INFORMATION:
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  ANTITHROMBOSIS AGENTS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/614,443A
;      FILING DATE:  19901116
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22803-20003.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-614-443A-2

  Query Match             30.4%;  Score 211.5;  DB 1;  Length 117;
  Best Local Similarity   36.9%;  Pred. No. 2.9e-18;
  Matches   45;  Conservative   28;  Mismatches   42;  Indels    7;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| : :||: |:|||||  ||:||::|  ||||:|  :: |  |: ::|  :
Db          1 DCPSDWSSYEGHCYRVFQQEMTWDDAEKFCTQQHTGGHLVSFRSSEEVDFLVSILKFDLF 60

Qy         63 YL-TRYIWIGLRVQ-NKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ::  | ||   |:| : |   : ::|:      || :| | |   :|    | : |: :|
Db         61 WMGWRDIWNERRLQWSDG---TKVNYKAWSAEPEC-IVCRATD-NQWLSTSCSKTHNVVC 115

Qy        121 KF 122
              ||
Db        116 KF 117


RESULT 23
US-08-294-859-2
; Sequence 2, Application US/08294859
; Patent No. 5679542
;  GENERAL INFORMATION:
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  ANTITHROMBOSIS AGENTS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/294,859
;      FILING DATE:  29-AUG-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2803-0003.10
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-294-859-2

  Query Match            30.4%;  Score 211.5;  DB 1;  Length 117;
  Best Local Similarity  36.9%;  Pred. No. 2.9e-18;
  Matches   45;  Conservative   28;  Mismatches   42;  Indels    7;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|:|| ||| : :||: |:|||||  ||:||::|  ||||:|  :: |  |: ::|  :
Db          1 DCPSDWSSYEGHCYRVFQQEMTWDDAEKFCTQQHTGGHLVSFRSSEEVDFLVSILKFDLF 60

Qy         63 YL-TRYIWIGLRVQ-NKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ::  | ||   |:| : |   : ::|:      || :| | |   :|    | : |: :|
Db         61 WMGWRDIWNERRLQWSDG---TKVNYKAWSAEPEC-IVCRATD-NQWLSTSCSKTHNVVC 115

Qy        121 KF 122
             ||
Db        116 KF 117


RESULT 24
US-08-481-676-2
; Sequence 2, Application US/08481676
; Patent No. 5744584
;  GENERAL INFORMATION:
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  ANTITHROMBOSIS AGENTS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,676
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/294,859
;      FILING DATE:  29-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2803-0003.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-481-676-2

  Query Match            30.4%;  Score 211.5;  DB 1;  Length 117;
  Best Local Similarity  36.9%;  Pred. No. 2.9e-18;
  Matches   45;  Conservative   28;  Mismatches   42;  Indels    7;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :|:|| ||| : :||: |:|||||  ||:||::|  ||||:|  :: |  |: ::|  :
Db          1 DCPSDWSSYEGHCYRVFQQEMTWDDAEKFCTQQHTGGHLVSFRSSEEVDFLVSILKFDLF 60

Qy         63 YL-TRYIWIGLRVQ-NKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQQHSFIC 120
              ::  | ||   |:| : |   : ::|:      || :| | |   :|    | : |: :|
Db         61 WMGWRDIWNERRLQWSDG---TKVNYKAWSAEPEC-IVCRATD-NQWLSTSCSKTHNVVC 115

Qy        121 KF 122
             ||
Db        116 KF 117


RESULT 25
US-08-612-840A-1
; Sequence 1, Application US/08612840A
; Patent No. 5856126
;  GENERAL INFORMATION:
;    APPLICANT:  FUKUCHI, Naoyuki
;    APPLICANT:  YAMAMOTO, Hiroshi
;    APPLICANT:  NAGANO, Mitsuyo
;    APPLICANT:  KITO, Morikazu
;    APPLICANT:  TANAKA, Akiko
;    APPLICANT:  ISHII, Koichi
;    APPLICANT:  KOBAYASHI, Tsuyoshi
;    APPLICANT:  YOSHIMOTO, Ryota
;    TITLE OF INVENTION:  PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
;    TITLE OF INVENTION:  METHOD OF PRODUCING THE SAME
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,840A
;      FILING DATE:  20-MAR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-236975
;      FILING DATE:  22-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5856126man F. Oblon
;      REGISTRATION NUMBER:  24,618
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  38 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-612-840A-1

  Query Match            29.9%;  Score 208;  DB 2;  Length 38;
  Best Local Similarity  94.7%;  Pred. No. 1.8e-18;
  Matches   36;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DLECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKG 38
              |||||||||| |||||||||||||| ||||||||||
Db          1 DLECPSGWSSYDRYCYKPFKQEMTWADAERFCSEQAKG 38
```

```
RESULT 26
US-07-893-929A-6
; Sequence 6, Application US/07893929A
; Patent No. 5336667
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/893,929A
;      FILING DATE:  19920605
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  No. 5336667e
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-893-929A-6

  Query Match             28.8%;  Score 200;  DB 1;  Length 107;
  Best Local Similarity   34.6%;  Pred. No. 6.8e-17;
  Matches   44;  Conservative   18;  Mismatches   37;  Indels   28;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| | |||| |:| | |  ||:|| :|  | |||| :: :| ||
Db          1 DCPSDWSSYDLYCYKVFQQRMNWEDAEQFCRQQHTGSHLLSFHSSEKADFV--------- 51

Qy         63 YLTRYIWIGL-------RVQ-NKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQ 114
                    ||||       |:| : |   : : |       ||  ::  |   :|:   | :
Db         52 ------WIGLTDVWSACRLQWSDG---TELKYNAWTAESEC--IASKTTDNQWWTRSCSK 100

Qy        115 QHSFICK 121
                : |:||
Db        101 TYPFVCK 107


RESULT 27
PCT-US92-10344-6
; Sequence 6, Application PC/TUS9210344
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10344
;      FILING DATE:  19921201
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
PCT-US92-10344-6

  Query Match             28.8%;  Score 200;  DB 5;  Length 107;
  Best Local Similarity   34.6%;  Pred. No. 6.8e-17;
  Matches   44;  Conservative   18;  Mismatches   37;  Indels   28;  Gaps    5;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKE 62
              :||| ||| | |||| |:| | |  ||:|| :|  | |||| :: :| ||
Db          1 DCPSDWSSYDLYCYKVFQQRMNWEDAEQFCRQQHTGSHLLSFHSSEKADFV--------- 51

Qy         63 YLTRYIWIGL-------RVQ-NKGQPCSSISYENLVDPFECFMVSRDTRLREWFKVDCEQ 114
                    ||||       |:| : |   : : |       ||  ::  |   :|:   | :
Db         52 ------WIGLTDVWSACRLQWSDG---TELKYNAWTAESEC--IASKTTDNQWWTRSCSK 100

Qy        115 QHSFICK 121
                : |:||
Db        101 TYPFVCK 107


RESULT 28
US-07-893-929A-3
; Sequence 3, Application US/07893929A
; Patent No. 5336667
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
```

```
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/893,929A
;       FILING DATE:  19920605
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/803,630
;       FILING DATE:  December 3, 1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Monaco, Daniel A.
;       REGISTRATION NUMBER:  30,480
;       REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 568-8383
;       TELEFAX:  (215) 568-5549
;       TELEX:  No. 5336667e
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  125 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  linear
US-07-893-929A-3

  Query Match             27.1%;  Score 188.5;  DB 1;  Length 125;
  Best Local Similarity   33.3%;  Pred. No. 2.2e-15;
  Matches   42;  Conservative   22;  Mismatches   49;  Indels   13;  Gaps    5;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              || |||| : |||| : ::| |  || || || |  ||:|  :: |  || :  :    |
Db          4 CPFGWSSYEGYCYKVYNKKMNWEDAESFCREQHKRSHLVSFHSSGEVDFVVSKTFPILRY 63

Qy         64 LTRYIWIGLRVQNKGQPCSS-------ISYENLVDPFECFMVSRDTRLREWFKVDCEQQH 116
                ::|:||   :  : |:        : |:       | :||: |   ||  :|| :
Db         64 --DFVWMGL--SDIWKECTKEWSDGARLDYKAWSGKSYC-LVSKTTN-NEWLSMDCSRTL 117

Qy        117 SFICKF 122
                :|||
Db        118 YPVCKF 123


RESULT 29
PCT-US92-10344-3
; Sequence 3, Application PC/TUS9210344
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10344
;      FILING DATE:  19921201
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  125 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
PCT-US92-10344-3

  Query Match             27.1%;  Score 188.5;  DB 5;  Length 125;
  Best Local Similarity   33.3%;  Pred. No. 2.2e-15;
  Matches   42;  Conservative   22;  Mismatches   49;  Indels   13;  Gaps    5;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANKEY 63
              || |||| : |||| : ::| |  || || || |  ||:|  :: |  || :  :    |
Db          4 CPFGWSSYEGYCYKVYNKKMNWEDAESFCREQHKRSHLVSFHSSGEVDFVVSKTFPILRY 63

Qy         64 LTRYIWIGLRVQNKGQPCSS-------ISYENLVDPFECFMVSRDTRLREWFKVDCEQQH 116
                ::|:||   :  : |:        : |:       | :||: |   ||  :|| :
Db         64 --DFVWMGL--SDIWKECTKEWSDGARLDYKAWSGKSYC-LVSKTTN-NEWLSMDCSRTL 117

Qy        117 SFICKF 122
                :|||
Db        118 YPVCKF 123


RESULT 30
US-09-949-016-10685
; Sequence 10685, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10685
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10685

  Query Match             24.2%;  Score 168;  DB 4;  Length 144;
  Best Local Similarity   31.1%;  Pred. No. 8.9e-13;
  Matches   42;  Conservative   25;  Mismatches   50;  Indels   18;  Gaps    5;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || | ::   |||   :   ||  |: :| :    |:|:|| |  | :|| :::   |
Db         12 ISCPEGTNAYRSYCYYFNEDRETWVDADLYC-QNMNSGNLVSVLTQAEGAFVASLI---K 67

Qy         62 EYLTR--YIWIGLRVQNKGQ-----PCSSISYE-------NLVDPFECFMVSRDTRLREW 107
              |  |    :||||    | :        | :||:       : |:|  |  ::  |  ::|
Db         68 ESGTDDFNVWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKW 127

Qy        108 FKVDCEQQHSFICKF 122
               | || : ||:|||
Db        128 KDVPCEDKFSFVCKF 142
```

```
RESULT 31
US-09-949-016-6286
; Sequence 6286, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6286
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-6286

  Query Match             24.2%;  Score 168;  DB 4;  Length 166;
  Best Local Similarity   31.1%;  Pred. No. 1.1e-12;
  Matches   42;  Conservative   25;  Mismatches   50;  Indels   18;  Gaps    5;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || | ::   |||   :   ||  |: :| :    |:|:|| |  | :|| :::   |
Db         34 ISCPEGTNAYRSYCYYFNEDRETWVDADLYC-QNMNSGNLVSVLTQAEGAFVASLI---K 89

Qy         62 EYLTR--YIWIGLRVQNKGQ-----PCSSISYE-------NLVDPFECFMVSRDTRLREW 107
              |  |    :||||    | :       | :||:       : |:|  |  ::  |  ::|
Db         90 ESGTDDFNVWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKW 149

Qy        108 FKVDCEQQHSFICKF 122
               | || : ||:|||
Db        150 KDVPCEDKFSFVCKF 164


RESULT 32
US-07-614-443A-5
; Sequence 5, Application US/07614443A
; Patent No. 5342830
;  GENERAL INFORMATION:
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  ANTITHROMBOSIS AGENTS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/614,443A
;      FILING DATE:  19901116
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22803-20003.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-614-443A-5

  Query Match             23.6%;  Score 164;  DB 1;  Length 50;
  Best Local Similarity   54.0%;  Pred. No. 6.8e-13;
  Matches   27;  Conservative   10;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASF 52
              :||| ||| : :||| |    ||  ||:||:||| ||||:|:::  ||:|
Db          1 DCPSDWSSHEGHCYKVFNLYKTWEDAEKFCTEQANGGHLVSIDSKKEANF 50


RESULT 33
US-08-294-859-5
; Sequence 5, Application US/08294859
; Patent No. 5679542
;  GENERAL INFORMATION:
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  ANTITHROMBOSIS AGENTS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/294,859
;      FILING DATE:  29-AUG-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2803-0003.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-294-859-5

  Query Match             23.6%;  Score 164;  DB 1;  Length 50;
  Best Local Similarity   54.0%;  Pred. No. 6.8e-13;
  Matches   27;  Conservative   10;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASF 52
              :||| ||| : :||| |    ||  ||:||:||| ||||:|:::  ||:|
Db          1 DCPSDWSSHEGHCYKVFNLYKTWEDAEKFCTEQANGGHLVSIDSKKEANF 50


RESULT 34
US-08-481-676-5
; Sequence 5, Application US/08481676
; Patent No. 5744584
;  GENERAL INFORMATION:
;    APPLICANT:  SCARBOROUGH, ROBERT M.
;    TITLE OF INVENTION:  ANTITHROMBOSIS AGENTS
```

```
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,676
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/294,859
;      FILING DATE:  29-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  2803-0003.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 887-0763
;      TELEX:  90-4030
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-481-676-5

  Query Match           23.6%;  Score 164;  DB 1;  Length 50;
  Best Local Similarity   54.0%;  Pred. No. 6.8e-13;
  Matches   27;  Conservative   10;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASF 52
              :||| ||| : :||| |    ||  ||:||:||| ||||:|::: ||:|
Db          1 DCPSDWSSHEGHCYKVFNLYKTWEDAEKFCTEQANGGHLVSIDSKKEANF 50


RESULT 35
US-08-401-530A-3
; Sequence 3, Application US/08401530A
; Patent No. 5834590
;  GENERAL INFORMATION:
;    APPLICANT:  Vinik, Aaron I.
;    APPLICANT:  Pittenger, Gary L.
;    APPLICANT:  Rafaeloff, Ronit
;    APPLICANT:  Rosenberg, Lawrence
;    APPLICANT:  Duguid, William P.
;    TITLE OF INVENTION:  INGAP PROTEIN INVOLVED IN PANCREATIC
;    TITLE OF INVENTION:  ISLET NEOGENESIS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Allegretti
;      STREET:  1001 G Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/401,530A
;      FILING DATE:  22-FEB-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kagan, Sarah A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  00570.48743
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  175 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Rattus rattus
US-08-401-530A-3

  Query Match           23.4%;  Score 162.5;  DB 2;  Length 175;
  Best Local Similarity   30.9%;  Pred. No. 5.5e-12;
  Matches   43;  Conservative   21;  Mismatches   56;  Indels   19;  Gaps    5;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || | :   |||  |:   ||  ||  | :: : |||:||    ||||: ::: |
Db         38 ISCPKGSQAYGSYCYALFQIPQTWFDAELACQKRPE-GHLVSVLNVAEASFLASMV-KNT 95

Qy         62 EYLTRYIWIGLRVQN-KGQPCSS---------ISYEN-------LVDPFECFMVSRDTRL 104
                :||||||      |:|             ::| |       :|   | :|| :
Db         96 GNSYQYIWIGLHDPTLGGEPNGGGWEWSNNDIMNYVNWERNPSTALDRGFCGSLSRSSGF 155

Qy        105 REWFKVDCEQQHSFICKFT 123
                |    || :  ::||||
Db        156 LRWRDTTCEVKLPYVCKFT 174


RESULT 36
US-08-709-662-3
; Sequence 3, Application US/08709662
; Patent No. 5840531
;  GENERAL INFORMATION:
;    APPLICANT:  Vinik, Aaron I.
;    APPLICANT:  Pittenger, Gary L.
;    APPLICANT:  Rafaeloff, Ronit
;    APPLICANT:  Rosenberg, Lawrence
;    APPLICANT:  Duguid, William P.
;    TITLE OF INVENTION:  INGAP PROTEIN INVOLVED IN PANCREATIC
;    TITLE OF INVENTION:  ISLET NEOGENESIS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  1001 G Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,662
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kagan, Sarah A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  00570.59178
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  175 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Rattus rattus
US-08-709-662-3

  Query Match             23.4%;  Score 162.5;  DB 2;  Length 175;
  Best Local Similarity   30.9%;  Pred. No. 5.5e-12;
  Matches   43;  Conservative   21;  Mismatches   56;  Indels   19;  Gaps    5;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || |  :   |||  |:   ||  ||  | :: : |||:||    ||||: :::  |
Db         38 ISCPKGSQAYGSYCYALFQIPQTWFDAELACQKRPE-GHLVSVLNVAEASFLASMV-KNT 95

Qy         62 EYLTRYIWIGLRVQN-KGQPCSS---------ISYEN-------LVDPFECFMVSRDTRL 104
                :||||||       |:|            ::| |        :|    |  :|| :
Db         96 GNSYQYIWIGLHDPTLGGEPNGGGWEWSNNDIMNYVNWERNPSTALDRGFCGSLSRSSGF 155

Qy        105 REWFKVDCEQQHSFICKFT 123
                |    || :  ::||||
Db        156 LRWRDTTCEVKLPYVCKFT 174


RESULT 37
US-07-893-929A-10
; Sequence 10, Application US/07893929A
; Patent No. 5336667
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/893,929A
;      FILING DATE:  19920605
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  No. 5336667e
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
US-07-893-929A-10

  Query Match             22.7%;  Score 158;  DB 1;  Length 123;
  Best Local Similarity   28.6%;  Pred. No. 1.2e-11;
  Matches   36;  Conservative   18;  Mismatches   60;  Indels   12;  Gaps    4;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETA-LEASFVDNVLYANKE 62
              |   ||  : |||| ||: | || ||:|| :| | |||:|   :
Db          2 CLPDWSVYEGYCYKVFKERMNWADAEKFCMKQVKDGHLVSFRNSKXXXXXXXXXXXXXXX 61

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKVDCEQQ 115
                 :||||   :  : |       : : |:   :   ||  :  |   :| :  |  :
Db         62 XKMELVWIGL--SDYWRDCYWEWSDGAQLDYKAWDNERHCF--AAKTTDNQWMRRKCSGE 117

Qy        116 HSFICK 121
                 |:||
Db        118 FYFVCK 123


RESULT 38
PCT-US92-10344-10
; Sequence 10, Application PC/TUS9210344
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10344
;      FILING DATE:  19921201
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
PCT-US92-10344-10

  Query Match             22.7%;  Score 158;  DB 5;  Length 123;
  Best Local Similarity   28.6%;  Pred. No. 1.2e-11;
  Matches   36;  Conservative   18;  Mismatches   60;  Indels   12;  Gaps    4;

Qy          4 CPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETA-LEASFVDNVLYANKE 62
              |   ||  : |||| ||: | || ||:|| :| | |||:|   :
Db          2 CLPDWSVYEGYCYKVFKERMNWADAEKFCMKQVKDGHLVSFRNSKXXXXXXXXXXXXXXX 61

Qy         63 YLTRYIWIGLRVQNKGQPC-------SSISYENLVDPFECFMVSRDTRLREWFKVDCEQQ 115
                 :||||   :  : |       : : |:   :   ||  :  |   :| :  |  :
Db         62 XKMELVWIGL--SDYWRDCYWEWSDGAQLDYKAWDNERHCF--AAKTTDNQWMRRKCSGE 117
```

```
Qy        116 HSFICK 121
                |:||
Db        118 FYFVCK 123


RESULT 39
US-08-464-637-2
; Sequence 2, Application US/08464637
; Patent No. 5834214
;  GENERAL INFORMATION:
;    APPLICANT:  Iovanna, Juan-Lucio
;    APPLICANT:  Dagorn, Jean-Charles
;    APPLICANT:  Keim, Volker
;    APPLICANT:  Sarles, Jacques
;    TITLE OF INVENTION:  Detection of Pancreatitis-Associated
;    TITLE OF INVENTION:  Protein for Diagnosis of Cystic Fibrosis or Pancreatic
;    TITLE OF INVENTION:  Disease (as amended).
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:. Birch, Stewart, Kolasch & Birch, LLP
;      STREET:  P.O. Box 747
;      CITY:  Falls Church
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22040-3487
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,637
;      FILING DATE:  30-AUG-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy Jr., Gerald M.
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  2121-107P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-205-8000
;      TELEFAX:  703-205-8050
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  175 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-464-637-2

  Query Match             22.1%;  Score 153.5;  DB 2;  Length 175;
  Best Local Similarity   25.7%;  Pred. No. 7.1e-11;
  Matches   36;  Conservative   24;  Mismatches   59;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :   :||  |   :|  |:  | ::   |:|:|| :  | ||| ::: :
Db         38 IRCPKGSKAYGSHCYALFLSPKSWTDADLAC-QKRPSGNLVSVLSGAEGSFVSSLVKSIG 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                |  |:||||    :|   :   :|                :  |  |  :|| |
Db         97 NSY--SYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYFAWERNPSTISSPGHCASLSRSTA 154

Qy        104 LREWFKVDCEQQHSFICKFT 123
                |   :|  :  ::||||
Db        155 FLRWKDYNCNVRLPYVCKFT 174


RESULT 40
US-08-401-530A-4
; Sequence 4, Application US/08401530A
; Patent No. 5834590
;  GENERAL INFORMATION:
;    APPLICANT:  Vinik, Aaron I.
;    APPLICANT:  Pittenger, Gary L.
;    APPLICANT:  Rafaeloff, Ronit
;    APPLICANT:  Rosenberg, Lawrence
;    APPLICANT:  Duguid, William P.
;    TITLE OF INVENTION:  INGAP PROTEIN INVOLVED IN PANCREATIC
;    TITLE OF INVENTION:  ISLET NEOGENESIS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Allegretti
;      STREET:  1001 G Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/401,530A
;      FILING DATE:  22-FEB-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kagan, Sarah A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  00570.48743
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  175 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-08-401-530A-4

  Query Match             22.1%;  Score 153.5;  DB 2;  Length 175;
  Best Local Similarity   25.7%;  Pred. No. 7.1e-11;
  Matches   36;  Conservative   24;  Mismatches   59;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :   :||  |   :|  |:  | ::   |:|:|| :  | ||| ::: :
Db         38 IRCPKGSKAYGSHCYALFLSPKSWTDADLAC-QKRPSGNLVSVLSGAEGSFVSSLVKSIG 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                |  |:||||    :|   :   :|                :  |  |  :|| |
Db         97 NSY--SYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYFAWERNPSTISSPGHCASLSRSTA 154

Qy        104 LREWFKVDCEQQHSFICKFT 123
                |   :|  :  ::||||
Db        155 FLRWKDYNCNVRLPYVCKFT 174


RESULT 41
US-08-709-662-4
; Sequence 4, Application US/08709662
; Patent No. 5840531
;  GENERAL INFORMATION:
;    APPLICANT:  Vinik, Aaron I.
;    APPLICANT:  Pittenger, Gary L.
;    APPLICANT:  Rafaeloff, Ronit
;    APPLICANT:  Rosenberg, Lawrence
;    APPLICANT:  Duguid, William P.
;    TITLE OF INVENTION:  INGAP PROTEIN INVOLVED IN PANCREATIC
;    TITLE OF INVENTION:  ISLET NEOGENESIS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  1001 G Street, N.W.
;      CITY:  Washington
```

```
;       STATE:  D.C.
;       COUNTRY:  US
;       ZIP:  20001-4597
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/709,662
;       FILING DATE:  09-SEP-1996
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kagan, Sarah A.
;       REGISTRATION NUMBER:  32,141
;       REFERENCE/DOCKET NUMBER:  00570.59178
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-508-9100
;       TELEFAX:  202-508-9299
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  175 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
US-08-709-662-4

  Query Match             22.1%;  Score 153.5;  DB 2;  Length 175;
  Best Local Similarity   25.7%;  Pred. No. 7.1e-11;
  Matches   36;  Conservative   24;  Mismatches   59;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :   :||  |    :|  |:  | ::   |:|:|| :  | ||| ::: :
Db         38 IRCPKGSKAYGSHCYALFLSPKSWTDADLAC-QKRPSGNLVSVLSGAEGSFVSSLVKSIG 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                |   |:||||    :|   :   :|                :  |  |  :|| |
Db         97 NSY--SYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYFAWERNPSTISSPGHCASLSRSTA 154

Qy        104 LREWFKVDCEQQHSFICKFT 123
                |   :|  :  ::||||
Db        155 FLRWKDYNCNVRLPYVCKFT 174


RESULT 42
US-08-822-261-3
; Sequence 3, Application US/08822261
; Patent No. 5935813
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN PANCEATITIS-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/822,261
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0251 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  175 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  262369
US-08-822-261-3

  Query Match             22.1%;  Score 153.5;  DB 2;  Length 175;
  Best Local Similarity   25.7%;  Pred. No. 7.1e-11;
  Matches   36;  Conservative   24;  Mismatches   59;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :   :||  |    :|  |:  | ::   |:|:|| :  | ||| ::: :
Db         38 IRCPKGSKAYGSHCYALFLSPKSWTDADLAC-QKRPSGNLVSVLSGAEGSFVSSLVKSIG 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
                |   |:||||    :|   :   :|                :  |  |  :|| |
Db         97 NSY--SYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYFAWERNPSTISSPGHCASLSRSTA 154

Qy        104 LREWFKVDCEQQHSFICKFT 123
                |   :|  :  ::||||
Db        155 FLRWKDYNCNVRLPYVCKFT 174


RESULT 43
US-09-226-852-3
; Sequence 3, Application US/09226852
; Patent No. 6492499
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN PANCEATITIS-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/226,852
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/822,261
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0251 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
```

```
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  175 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  262369
US-09-226-852-3

  Query Match             22.1%;  Score 153.5;  DB 4;  Length 175;
  Best Local Similarity   25.7%;  Pred. No. 7.1e-11;
  Matches   36;  Conservative   24;  Mismatches   59;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :   :|| |    :|  |:  | ::   |:|:|| :  | ||| ::: :
Db         38 IRCPKGSKAYGSHCYALFLSPKSWTDADLAC-QKRPSGNLVSVLSGAEGSFVSSLVKSIG 96

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE-----------------NLVDPFECFMVSRDTR 103
                |   |:||||    :|   :   :|                  :  |  |  :|| |
Db         97 NSY--SYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYFAWERNPSTISSPGHCASLSRSTA 154

Qy        104 LREWFKVDCEQQHSFICKFT 123
                |   :|  :  ::||||
Db        155 FLRWKDYNCNVRLPYVCKFT 174


RESULT 44
US-09-949-016-10537
; Sequence 10537, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10537
;   LENGTH: 183
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10537

  Query Match             22.1%;  Score 153.5;  DB 4;  Length 183;
  Best Local Similarity   25.7%;  Pred. No. 7.5e-11;
  Matches   36;  Conservative   24;  Mismatches   59;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :   :|| |    :|  |:  | ::   |:|:|| :  | ||| ::: :
Db         46 IRCPKGSKAYGSHCYALFLSPKSWTDADLAC-QKRPSGNLVSVLSGAEGSFVSSLVKSIG 104

Qy         61 KEYLTRYIWIGLRVQNKGQPCSSISYE-----------------NLVDPFECFMVSRDTR 103
                |   |:||||    :|   :   :|                  :  |  |  :|| |
Db        105 NSY--SYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYFAWERNPSTISSPGHCASLSRSTA 162

Qy        104 LREWFKVDCEQQHSFICKFT 123
                |   :|  :  ::||||
Db        163 FLRWKDYNCNVRLPYVCKFT 182


RESULT 45
US-08-401-530A-7
; Sequence 7, Application US/08401530A
; Patent No. 5834590
;  GENERAL INFORMATION:
;    APPLICANT:  Vinik, Aaron I.
;    APPLICANT:  Pittenger, Gary L.
;    APPLICANT:  Rafaeloff, Ronit
;    APPLICANT:  Rosenberg, Lawrence
;    APPLICANT:  Duguid, William P.
;    TITLE OF INVENTION:  INGAP PROTEIN INVOLVED IN PANCREATIC
;    TITLE OF INVENTION:  ISLET NEOGENESIS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Allegretti
;      STREET:  1001 G Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/401,530A
;      FILING DATE:  22-FEB-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kagan, Sarah A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  00570.48743
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  165 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Rattus rattus
US-08-401-530A-7

  Query Match             21.7%;  Score 151;  DB 2;  Length 165;
  Best Local Similarity   29.6%;  Pred. No. 1.3e-10;
  Matches   40;  Conservative   26;  Mismatches   51;  Indels   18;  Gaps    5;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || | ::   |||   :  ::|| |: || :    |:|:|| :  | :|: :::   |
Db         33 ITCPEGSNAYSSYCYYFMEDHLSWAEADLFC-QNMNSGYLVSVLSQAEGNFLASLI---K 88

Qy         62 EYLT--RYIWIGLR--VQNKGQPCSSIS----------YENLVDPFECFMVSRDTRLREW 107
              | |    :||||      |:    || |           | |  :   |  |: ::  ::|
Db         89 ESGTTAANVWIGLHDPKNNRRWHWSSGSLFLYKSWDTGYPNNSNRGYCVSVTSNSGYKKW 148

Qy        108 FKVDCEQQHSFICKF 122
                |: | ||:|||
Db        149 RDNSCDAQLSFVCKF 163


RESULT 46
US-08-729-103-3
; Sequence 3, Application US/08729103
; Patent No. 5837841
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN REG PROTEIN
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
```

```
;       STATE:  CA
;       COUNTRY:  US
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/729,103
;       FILING DATE:  Filed Herewith
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0138 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  165 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:  GenBank
;       CLONE:  393209
US-08-729-103-3

  Query Match             21.7%;  Score 151;  DB 2;  Length 165;
  Best Local Similarity   29.6%;  Pred. No. 1.3e-10;
  Matches   40;  Conservative   26;  Mismatches   51;  Indels   18;  Gaps    5;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || | ::   |||   :  ::|| |: || :    |:|:|| :  | :|: :::   |
Db         33 ITCPEGSNAYSSYCYYFMEDHLSWAEADLFC-QNMNSGYLVSVLSQAEGNFLASLI---K 88

Qy         62 EYLT--RYIWIGLR--VQNKGQPCSSIS----------YENLVDPFECFMVSRDTRLREW 107
              |  |    :||||     |:    || |          | |  :   |  |: ::  ::|
Db         89 ESGTTAANVWIGLHDPKNNRRWHWSSGSLFLYKSWDTGYPNNSNRGYCVSVTSNSGYKKW 148

Qy        108 FKVDCEQQHSFICKF 122
              |: | ||:|||
Db        149 RDNSCDAQLSFVCKF 163


RESULT 47
US-08-709-662-7
; Sequence 7, Application US/08709662
; Patent No. 5840531
;  GENERAL INFORMATION:
;    APPLICANT:  Vinik, Aaron I.
;    APPLICANT:  Pittenger, Gary L.
;    APPLICANT:  Rafaeloff, Ronit
;    APPLICANT:  Rosenberg, Lawrence
;    APPLICANT:  Duguid, William P.
;    TITLE OF INVENTION:  INGAP PROTEIN INVOLVED IN PANCREATIC
;    TITLE OF INVENTION:  ISLET NEOGENESIS
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Banner & Witcoff, Ltd.
;      STREET:  1001 G Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  US
;      ZIP:  20001-4597
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,662
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kagan, Sarah A.
;      REGISTRATION NUMBER:  32,141
;      REFERENCE/DOCKET NUMBER:  00570.59178
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-508-9100
;      TELEFAX:  202-508-9299
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  165 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Rattus rattus
US-08-709-662-7

  Query Match             21.7%;  Score 151;  DB 2;  Length 165;
  Best Local Similarity   29.6%;  Pred. No. 1.3e-10;
  Matches   40;  Conservative   26;  Mismatches   51;  Indels   18;  Gaps    5;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYANK 61
              : || | ::   |||   :  ::|| |: || :    |:|:|| :  | :|: :::   |
Db         33 ITCPEGSNAYSSYCYYFMEDHLSWAEADLFC-QNMNSGYLVSVLSQAEGNFLASLI---K 88

Qy         62 EYLT--RYIWIGLR--VQNKGQPCSSIS----------YENLVDPFECFMVSRDTRLREW 107
              |  |    :||||     |:    || |          | |  :   |  |: ::  ::|
Db         89 ESGTTAANVWIGLHDPKNNRRWHWSSGSLFLYKSWDTGYPNNSNRGYCVSVTSNSGYKKW 148

Qy        108 FKVDCEQQHSFICKF 122
              |: | ||:|||
Db        149 RDNSCDAQLSFVCKF 163


RESULT 48
US-07-893-929A-8
; Sequence 8, Application US/07893929A
; Patent No. 5336667
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/893,929A
;      FILING DATE:  19920605
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
```

```
;       REGISTRATION NUMBER:  30,480
;       REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (215) 568-8383
;       TELEFAX:  (215) 568-5549
;       TELEX:  No. 5336667e
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  128 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  linear
US-07-893-929A-8

  Query Match             21.4%;  Score 148.5;  DB 1;  Length 128;
  Best Local Similarity   27.3%;  Pred. No. 1.9e-10;
  Matches   35;  Conservative   11;  Mismatches   73;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFV-DNVLYANK 61
              :||| ||| | |||| |:: | |  ||:|| :|  |        :: |  ||
Db          1 DCPSDWSSYDLYCYKVFQERMNWEDAEQFCRQQHTGXXXXXXHSSEEVDFVXXXXXXXXX 60

Qy         62 EYLTRYIWIGLRVQNKGQPC--------SSISYENLVDPFECFMVSRDTRLREWFKVDCE 113
                 ||||          |             ||             :   |
Db         61 XXXXXXXWIGLTDVXXWSACRLQWSDGTELXKYNAWTAESECIASXXXXXXXXXWTRSCS 120

Qy        114 QQHSFICK 121
              : : |:||
Db        121 RTYPFVCK 128


RESULT 49
PCT-US92-10344-8
; Sequence 8, Application PC/TUS9210344
;  GENERAL INFORMATION:
;    APPLICANT:  Kirby, Edward P.
;    APPLICANT:  Peng, Man-ling
;    TITLE OF INVENTION:  Alboaggregins: Platelet
;    TITLE OF INVENTION:  Agonists Which Bind To Platelet
;    TITLE OF INVENTION:  Membrane Glycoprotein Ib
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Temple University - Of The Common-
;      ADDRESSEE:  wealth System of Higher Education
;      STREET:  406 University Services Building
;      CITY:  Philadelphia
;      STATE:  Pennsylvania
;      COUNTRY:  U.S.A.
;      ZIP:  19122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 720 Kb
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10344
;      FILING DATE:  19921201
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,630
;      FILING DATE:  December 3, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monaco, Daniel A.
;      REGISTRATION NUMBER:  30,480
;      REFERENCE/DOCKET NUMBER:  6056-126 (CIP) 1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-8383
;      TELEFAX:  (215) 568-5549
;      TELEX:  None
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  128 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
PCT-US92-10344-8

  Query Match             21.4%;  Score 148.5;  DB 5;  Length 128;
  Best Local Similarity   27.3%;  Pred. No. 1.9e-10;
  Matches   35;  Conservative   11;  Mismatches   73;  Indels    9;  Gaps    2;

Qy          3 ECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFV-DNVLYANK 61
              :||| ||| | |||| |:: | |  ||:|| :|  |        :: |  ||
Db          1 DCPSDWSSYDLYCYKVFQERMNWEDAEQFCRQQHTGXXXXXXHSSEEVDFVXXXXXXXXX 60

Qy         62 EYLTRYIWIGLRVQNKGQPC--------SSISYENLVDPFECFMVSRDTRLREWFKVDCE 113
                 ||||          |             ||             :   |
Db         61 XXXXXXXWIGLTDVXXWSACRLQWSDGTELXKYNAWTAESECIASXXXXXXXXXWTRSCS 120

Qy        114 QQHSFICK 121
              : : |:||
Db        121 RTYPFVCK 128


RESULT 50
US-08-822-261-1
; Sequence 1, Application US/08822261
; Patent No. 5935813
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN PANCEATITIS-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/822,261
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0251 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  175 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  ISLTNOT01
;      CLONE:  2072483
US-08-822-261-1

  Query Match             21.4%;  Score 148.5;  DB 2;  Length 175;
  Best Local Similarity   25.9%;  Pred. No. 2.9e-10;
  Matches   36;  Conservative   25;  Mismatches   57;  Indels   21;  Gaps    4;

Qy          2 LECPSGWSSTDRYCYKPFKQEMTWASAERFCSEQAKGGHLLSVETALEASFVDNVLYA-N 60
              : || |  :    ||  |    :|  |:  | ::   | |:|| :  | ||| ::: : :
Db         38 ISCPKGSKAYGSPCYALFLSPKSWMDADLAC-QKRPSGKLVSVLSGAEGSFVSSLVRSIS 96
```

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Qy          61 KEYLTRYIWIGLRVQNKGQPCSSISYE----------------NLVDPFECFMVSRDTR 103
               |   ||||||    :|       :|                  :::|  |  :|| |
Db          97 NSY--SYIWIGLHDPTQGSEPDGDGWEWSSTDVMNYFAWEKNPSTILNPGHCGSLSRSTG 154

Qy         104 LREWFKVDCEQQHSFICKF 122
                 :|   :|: :  ::|||
Db         155 FLKWKDYNCDAKLPYVCKF 173
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Search completed: May 2, 2005, 16:02:54
Job time : 26 secs